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Ibrahim, Medina A. Friday, November 01, 2002 8:29 PM STIC-Biotech/ChemLib 09/905, 558

Please search the following:

1. SEQ ID NO:3 and 16. Please search both commercial and issued patents databases. Thanks

Medina A. Ibrahim Patent Examiner GAU:1638 CM1-9A12 mailbox9E12 (703)306-5822

> Mary Jane Ruhl Tech. Info. Specialist, STIC TC-1600 CM-1, Room 6A-06 Phone: 605-1155

info. Specialist, STIC TC-1600 :W-1, Room 6A-06 hons: 605-1155

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where appl	ic.)
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Lexis/Nexis:	
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WWW/Internet:	
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Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:

Published_Applications_NA contains nucleic acid sequences; the search results will have the extension .rnpb.

Published_Applications_AA contains amino acid sequences; the search results will have the extension .rapb.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may requests that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

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1 (sites)
Conner,T.W., Dubois,P., Malven,M. and Masucci,J.D.
Plant regulatory sequences for selective control of gene expression Patent: WO 0183790-A 92 08-NOV-2001;
Monsanto Technology LLC (US)
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PAT 26-NOV-2001

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Submitted (24-MAY-1994) Young-Kwan Jin, Biological Sciences, Purdue
University, 339 Hansen Life Science Research Building, West
Lafayette, IN 47907, USA
Location/Qualifiers
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3722. .3844,3927. .4031,4113. .4257,4379. .4543,4637.
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Integration and Nonrandom Mutation of a Plasma Membrane Pr
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1 (bases 1 to 1889)
Anderson, H.M., Chay, C.A., Chen, G. and Conner, T.W.
Plant regulatory sequences for control of gene expression Patent: WO 0119976-A 65 22-MAR-2001;
MONSANTO COMPANY (US)
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                                           57;
               DB 6;
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Pred. No. 7.1e-19;
            Score 232.8; DB 6
Pred. No. 1.8e-44;
0; Mismatches 57
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Sequence 65 from Patent W00119976.
AX099709
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/db_xref="taxon:4577"
443 c 423 g
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Best Local Similarity 63.9%;
Matches 227; Conservative
               17.8%;
83.0%;
                                 Best Local Similarity 83.0
Matches 289; Conservative
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.3629, .4875, .5950,

exon 3927 .4031 /gene="Mhal" /number=11 /gene="Mhal" /gene="Mhal" /number=11 exon 4133 .4257 /gene="Mhal" /number=12 intron 4258 .4378 /gene="Mhal" /number=12	/number=13 intron 4544. 4636 /qene="Whal"	/number=13 46374875 /gene="Mhal"	uc	exon 4964. /gene="Mhal" /number=15 intron 4997. 5090	/ yeire	/number=16 intron 51735256 /gene="Mhal"	/number=16 52575417 /gene="Mha1"	//umber=1/ 5/18. :512 /gene="Mhal"	/number=17 6xon 55135689 /gene="Mhal"	intron 5690. 5767 /gene="Mhal" /numher=18		Intron 5951		_site 6408 /evidence-experimenta _site 6409 /evidence-experimenta	BASE COUNT 2329 a 2181 c 2086 g 2689 t ORIGIN	Query Match 8.6%; Score 112.2; DB 8; Length 9285; Best Local Similarity 74.1%; Pred. No. 8.8e-16; Matches 177; Conservative 0; Mismatches 43; Indels 19; Gaps	QY 78 CCGTTCGAGTGACTGCATGCGTACATCTTTCTGCATCGACCTTGTACGCTACATCGAA 137	
FVGITLLINSTISFIEENNAGNAAAALMARLAPKAKVLRNGRWAEEESAILVPGDI ISVKLGDIIPADARLLEGEDPLKIDQSALTGESLEYTKGFODGVYSGSTCKQGEIEAVV IATGWIFFEKAAALLVDSTNQVGHPQKVLTAIGNECICSTAVGMLVEILVWFPQIRA YRSGIDMLLVLLIGGIPTAMPTVLSVTAMIGAHRLAQOGAITKRWTAIEERAAGDILC SDKTGTLTLNOLTVDKSTLVSVTAMIGAHRLAQOGAITKRWTAIEERAAGDILC SDKTGTLTLNOLTVDKSTLVBPCRGVDQDTVILMAARASRTENQDAIDATIVGMLADP TEARAGVOEIHFLPFNPTDKRTALTILOGGGRWHWYSKGABGILHHRNKEDIETRV RAVIDNRARIGGOLAIGKETARRLGMGYNWYPSSAGLEPEPPERSOSONYKMITGOQLAIGKESPGGFWEFWGLLPEPPERSOSONYKMITGOQLAIGKESPGGFWEFWGLLPEPPERSOSONYKWITGOLAIGKETARRLGMGYNWYTTAVGSTIRALTAINGTAINAKPEPPEP VLIALUNGSTIWTISKDRVKPSPQPDSWKLAEIFATGVVLGTKLAMMTVIFFWAAYK TDFFPRLFHVSIAHDDFQMLAAAVTLQVSTISQALIFWTGTLALNKREPPEPP KLVAQLIATLINGSTIWTISKDRVKPSPQPDSWKLAEIFATGVVLGTKLAMMTVIFFWAAYK TDFFPRLFHVSIAHDDFQMLAAAVTLQVSTISQALIFWTSKRSWSFWEPRGFLLLVSA RLVAQLIATLIAVYANNARFAAIRGKGIGWGWAGVTNIVVYYLPLDIIKFLIRVAALGSR AWHLLLUGGRIAFTSKRNFGAEERRRWAHAQRSLHGLLDPPEAASMFENKTSFSEVN	OLABEARREMARSDCCLSSISTERGDQTLHCPV" 1509. 1873 /gene="Mhal"	/number=1 18741993 /gene="Mhal" /number=2	intron 19942104 /gene="Mhal" /number=2 exon 2105	// / / / / / / / / / / / / / / / / / /	/number=3 23162453 /gene="Mhal"	/number=4 intron 24542524 /gene="Mhal"	exon 2525. 2659 /gene="Mhal" /numhe==5	intron 2560. 2750 /gene="Mhal"	exon	<pre>intron 29313018 /gene="Mha1" /cons_splice=(5'site:no, 3'site:yes)</pre>	exon 30193225 /gen="mail"	intron 3226. 3305 /gene="Mhal"	exon 33063425 /gene="Mha1" /numher=A	uo		intron 5530. :3721 /gene="Mha1" /number=9 exon 37223844	/gene="Mhal" /number=10 /gene="Mhal" /number=10	

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AF429315
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Homo sapiens chromosome 4 clone RP11-439B3, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (26-JAN-2002) Genome Sequencing Center, Washington
Iniversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jan 31, 2002 this sequence version replaced gi:18376960.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 174802)
                         -----TC 119
                                                            GTAGGGTACATICTGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATAC 257
                                                                                               118 GCAGGGTACTTTTAAATTTCCATACTTGTGCAT-GTTTCATTTATGTTTACTACTTATGC 60
                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                         Sequencing vector: M13; 2%
Sequencing vector: plasmid; 98%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 17371 Dases at least Q40
Consensus quality: 173768 bases at least Q20
Insert size: 173000; agarose-fp
Insert size: 173000; agarose-fp
Insert size: 17402; sum-of-contigs
Quality coverage: 12.07 in Q20 bases; sum-of-contigs
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Center code: WUGSC
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HTG; HTGS_PHASE1; HTGS_FULLTOP
     160 CATACACACAGAGATGTCTCATGTGAATGGAGCCACTGATG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Homo sapiens clone
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Waterston, R.H.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Jases 1 to 125020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S.,
Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A.,
Potter, N.T., Ross, C.A. and Margolis, R.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 AAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 TTACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACATAGTCTACAATG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 TACATTCTGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAG 263
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4.6%; Score 60.2; DB 2; Length 174802;
Best Local Similarity 52.6%; Pred. No. 0.0035;
Matches 131; Conservative 0; Mismatches 118; Indels 0;
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
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6 24385: gap of unknown length (6 63017: contrig of 38632 bp in length 8 63177: gap of unknown length 8 113781: contig of 50664 bp in length 2 113881: gap of unknown length 2 174802: contig of 60921 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         1263. 2346
/note="assembly_name:Contig27"
2447. 8520
/note="assembly_name:Contig32"
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/note="assembly_name:Contig33"
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/note="assembly_name:Contig36"
33646 c 34740 g 50806 t
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/note="assembly_name:Contig35
                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
                                                                                                                                                                                                                                                                   clone="RP11-439B3"
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1165 CAGGICICCGCTCGCGTGCCTTCCAGTCTGTCTCACTAGCTGCTGTGGGACGATCGAA 1224
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Unpublished
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http://www.genomics.org.cn
                                                                                                                                                                      17432 SMKRRWWGKSAMYRMRRWWKGRGA 17455
                                                                                                                                                1285 GCTGATCAAGGGAAAGTGATCGGA 1308
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AC090043.1 GI:12745081
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Center code: Beljing
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AC090043
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HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWYKGEWTHGFKGRYGVRECAG
NGAKKEGTWSNGLQDGYGTETYSDG"
32731 c 30696 g 28283 t 4254 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="JPH3"
/note="component of the junctional complex between plasma
membrane and endoplasmic reticulum"
                                                                                2 (bases 1 to 125020)
Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission
Submisted (05-0CT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | : : : : : : : : : : : : : : : : | 16952 SKGWKWYSRGMSKSKSMRTGGSKWMRSSMMCTSSCYASMCCMCCWSCCCMRSCCCMRRS 17011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17072 GKGKGGKSYGRKTKRKSKGKMKGAKWYMYYRRSMRKMKMYSSKGMYCMYCWCWGRRGCYC 17131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16892 KSWMSWBMSVSYSVKMHSWHASBSCMHWBKCMTWSCCMSMMYKSSWWGSSWGMCCWGRRR 16951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 17132 SCMTSRSAMCCSYCYAKCKSMCYSCYYGMSMKGYYYACSYRGSWSSKYCMRGSTYSTSCG 17191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17192 CCCTTTTTCCCCCCNANTGGGGAAGCTTTTNCNKKTYSYYRKRNGCAMCKYNNYNNSWRS 17251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   985 GGACACCCGACACCCTGTCGGCCCTTTGTTTATTCCGGAAATCTCATCTGCCCCAC 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAACTTATTTGCCGTGCGCTCC 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805 GAGGIGGIGCCCCGIGCCCACICICCACGICCACGCACCAICCCICIGCAGCCGCICAC 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACGAAGGGCACTACCCCAACCTCTCACCGAAAAACCGCGCTGGATCGGCAAATCAAAC 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCCGTGCCCGTGCCGCTCCGCCAACGAGGCGGCCCGCGCGCTGCTGAGTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/noramcsone="15"
/mote="isolated from a patient with Huntington's Disease-Like 2 (HDL2)"
complement(35581. 35746)
         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.4%; Score 58.2; DB 9; Length 125020;
llarity 10.6%; Pred. No. 0.0096;
Conservative 248; Mismatches 256; Indels 0;
 A repeat expansion in the gene encoding junctophilin-3 associated with Huntington disease-like 2 Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                            /rpt_type=tandem
/rpt_unit=ctg
complement(<36507. .>36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                   /product="junctophilin 3"
complement(<36507, >36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"junctophilin 3"
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/db_xref-"GI:17646245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="JPH3
                                                                                                                                                                                            1. .125020
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="JP3
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Best Local S
Matches 60
                                                                 PUBMED
REFERENCE
AUTHORS
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ORIGIN
                                                                                                                                     JOURNAL
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.
I (bases 1 to 173848)
Xiong, H., Zhou, Y., Dong, H., Lin, W., Chen, B., Zhang, C., Zhang, Y., Cai, Z., Ying, H.F., Wang, H., Gu, W., Zhu, G., Tu, Y., Zhang, X., Jia, J., Shen, H., Zhang, D., Wu, C., Lu, G., Zhong, M., Jiang, H., Ren, S., Fu, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2. (bases 1 to 173848)
Bao,J., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,H., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,F., Li,F., Li,G., Li,T., Li,T., Li,X., Li,C., Li,C., Li,F., Li,Y., Li,W., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173848 bp DNA linear PRI 11-FEB-2001 chromosome 3 clone RP11-551L4 map 3p, complete
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Submitted (11-FEB-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
                                                                                                                                                                                         17312 KCCWCMKMCYCMMRSMRSRGMSYYMYASWKSSSRGCYCTRCYWCMSSKSCYKSYYMMMRS 17371
                                                                                                                     1225 GIGGGIGTCAGCTAGCTAGCTGCGCCGTGACCACGCACATGACCGCAGTGCGCGCGGG 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo saplens"
/db_xref="taxon:9606"
/chromosome="3"
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Query Match

Matches

280

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BASE COUNT ORIGIN

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http://www.sanger.ac.uk/HGP/Chr9
This sequence is the entire insert of clone RP11-382H24 The true .
This sequence is the entire insert of clone RP11-382H24 The true .
This sequence is the entire for at 135950 in this sequence. The true right end of clone RP11-187K14 is at 53851 in this sequence.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chamistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-382H24 is from the library RPCI-11.2 constructed by the group of Pleter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches 5583. .6152 of consensus"
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2452. .2801
//note="175 copies 2 mer ta 61% conserved"
2819. .2911
//note="LiMck repeat: matches 7864. .7961 of consensus"
complement(4102. .4478)
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Anote="MIR repeat: matches 1. .261 of consensus"

5200. 5294

Anote="L2 repeat: matches 2578. .2670 of consensus"

6031. .6654

Anote="L15A12 repeat: matches 5583. .6152 of consens

7419. 7966
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/note="LiMA7 repeat: matches 6223. .6284 of consens
LimA7 repeat: matches 6223. .6284 of consensus"
10099. .10533
/note="MLTIC repeat: matches 9. .466 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Alusc repeat: matches 1. .307 of consensus" 7763. 8103 https://matches.205. .536 of consens: 8379. .8422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: GSS: Em:AQ700717"
complement(1479. .2009)
/note="match: GSS: Em:AQ569033"
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7note="match: GSS: Em:AQ378047"
on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone="RP11-382H24"
/clone_lib="RPCI-11.2"
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Location/Qualifiers
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Lountied (04-DBC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries:

Cambridgeshire, CBIO 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jul 1, 2000 this sequence version replaced gi:8653807.

During sequence assembly data is comparated from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 04-DEC-2001
                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human DNA sequence from clone RP11-182H24 on chromosome 9p22.1-23 Contains a thioredoxin peroxidase pseudogene, a SSB (Sjogren syndrome antigen B (autoantigen La) pseudogene, the 3' end of the complete sequence.

ALIGIA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                 160 TGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCCGTAGGGTACATTCTGTTCTTCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 AAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTAT-TCTACAT 398
                                                                                                                                                                                                                                           100 TACATCTTTCTGCATCGACTTTGTACGGCTACATCGAACATATACACGAGATGTCTCGTG 159
                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 TATTIGIGCATATITITATIGITIGITIACTGATIATACGAGIAGITATACATACATGCAC
                                                                                                                                                                                          1;
                                                                                                                                   Length 173848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                          234; Indels
                                                                                                                                           DB 9;
                                                                                                                                                                    0.025
                                      /clone="RP11-551L4"
a 31451 c 31882 g 53852 t
                                                                                                                                                                                             0; Mismatches
                                                                                                                                         Score 56.6;
Pred. No. 0.
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Sehra, H.
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HTG; CpG island; MPDZ.
                                                                                                                                         tch 4.3%;
al Similarity 47.0%;
20%; Conservative
             /map="3p"
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LOCUS DEFINITION

AL161449 RESULT 7

Db 164129

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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AUTHORS
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comp.demnt(12572. .13167)
/gene="bA382H24.1" (thioredoxin peroxidase pseudogene)
/match: cDNAs: Em:UZ7125 Em:AF221841
match: proteins: Sw:091191 Tr:093241 Sw:006830 Sw:P32119
Sw:063716 Sw:P35704 Sw:090384 Tr:044366 Sw:P35700
Sw:Q61171 Tr:096763 Tr:061000 Tr:085761"
                                                                                                                                                                                                                                 /evidence=not_experimental
14831..15165
/note="match: STS: Em:HS260YA5"
14993..15030
/note="1672"
/note="MLT2D repeat: matches 1. .90 of consensus"
16759..16759..16739
/note="MLT1A1 repeat: matches 1. .241 of consensus"
17339..17638
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MLTIJ repeat: matches 33. .189 of consensus" 18882. .18943 /note="MLTIJ repeat: matches 411. .467 of consensus" 18886. .19291 /note="ALISx repeat: matches 1. .307 of consensus" 19450. .19635
                                                                                                                                                                                                                                                                                                                                                                /note="Alur repeat: matches 4. .304 of consensus" 7765. 18235 / 1065. 18235 / 1066="12 repeat: matches 1961. .2750 of consensus" 18526. 18676
10789. .11105
//note="Alusx repeat: matches 1. .309 of consensus"
11109. .11267
//note="matches 1. .178 of consensus"
complement(12290. .12569)
//note="match: STS: Em:005562"
complement(12572. .13167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .248 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 59. .248 of cr
20230. .20295
/note="33 copies 2 mer at 75% conserved"
complement(21475. .21909)
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// Anote="match: GSS: Em:B46263"
// 1040. 22231
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204652 bp DNA linear HTG 19-AUG-1999 Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN ALO49183 ***, in unordered pieces; ALO49183.5 GI:5763804 HTGS DUANTES D
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Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
On Aug 24, 1999 this sequence version replaced g1:5731886.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This
sequence is unfinished and does not necessarily represent the
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malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 204652)
Bowman.S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M.
130392. 30590

/note="L2 repeat: matches 1771. .1986 of consensus HERVL repeat: matches 5456. .5654 of consensus" 30591. .30631.

/note="MLT2B repeat: matches 1. .41 of consensus MLT2B. repeat: matches 1. .41 of consensus MLT2B. repeat: matches 1. .41 of consensus 30622. .31397

/note="L2 repeat: matches 1156. .1771 of consensus" 31401. .3187

/note="MLTH repeat: matches 13. .516 of consensus" 31936. .32142 repeat: matches 13. .516 of consensus" 700te="MLTH repeat: matches 13. .516 of consensus" 31936. .3214 repeat: matches 1. .297 of consensus" 700te="match: 658: Em:AQ799891" 32706. .3406

/note="match: 658: Em:AQ799891" 34145. .34705

/note="match: 658: Em:AQ350618

match: 578: Em:G57679" 35217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="1." repeat: matches 4928. .5057 of consensus" 35239. .36006
/note="LiMe1 repeat: matches 5352. .6103 of consensus" 37784. .37985
/note="LiMc4 repeat: matches 5695. .5897 of consensus"
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Rouhbakhsh,D., Lai,C.Y., von Dohlen,C.D., Clark,M.A., Baumann,L., Baumann,P., Moran,N.A. and Veegtlin,D.J.

The tryptophan biosynthetic pathway of aphid endosymbionts (Buchnera); genetics and evolution of plasmid-associated anthranilate synthase (trpEG) within the aphididae

J. Mol. Evol. 42 (4), 414-421 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 TACATTCTGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAG 263
correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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Submitted (20-58D-1995) Biological Sciences, Idaho State
University, Campus Box 8007, Pocatello, ID 83209, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                              /db_xref="taxon:5833"
/chromosome="13"
a 17396 c 17710 g 67856 t 32810 others
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                                                                                                                                                                                                                                                                                                                                                               Score 55.6; DB 2; LPred. No. 0.044;
                                                                                                                                                                                                                  1. .20465<u>5</u>
/organism="Plasmodium falciparum"
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/organelle="mitochondrion"
/db_xref="taxon:13262"
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Matches 121; Conservative
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PFMAL13P6 204652 bp DNA linear HTG 19-AUG-1999 Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
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/transl_table=5
/product="cytochrome oxidase subunit II"
/protein_id="cytochrome oxidase subunit II"
/db_xref="cytochrome" oxidase subunit II"
/db_xref="cytochrome" oxidase subunit III"
/ranslation="mynthisese subunit III"
/ranslation="mynthisese subunit III"
/ranslation="mynthisese subunit III"
/ranslation="mynthisese subunit III"
/db_xref="cytochrome" oxidase subunit III"
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HTG; HTGS_PHASE1.
HTG; HTGS_PHASE1.
Palasmodium falciparum.
Plasmodium falciparum aplicomplexa; Haemosporida; Plasmodium.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 204652)
Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 ACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATTGTTCTATTTCGAATT 414
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* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 CTACTCTACATCTTTCATATTCAATGAAATTAAT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"strong similarity to caffeoyl-CoA
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ED Arabidopsis sequencing, project.

Direct Submission

Submitted (12-MAR-1999) MIPS, at the Max-Planck-Institut fuer
Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosome 4 can be
Location/Qualifiers
                                                                                                                             ï
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(ESSA project).
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                                                                                                                                                                                             Db 154818 TAATAATAAAAATATATATATTCTTAATAAATTGAACACATTTTAATTTTACATTT 154759
                                                                                                                                                                                                                                                                         DD 154638 ATTATATTTGTATAGATTCTGAATTTAATGCCTATATGAAAAATTGATATTATT---AA 154582
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                                                                                                                                                     173 TAATGCCTTAAGCATGGGTTACTCCGTAGGGTACAITCTGTTCTTATTTGTGCATAT 232
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                                                                                                                                                                                                                                                                                                                                    293 CATATATCACAATATTTTTCTAAATTAAATTAAAACTAAAAATGACTAAATTTCTAACAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                           353 CAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATTGTTCTATTTCGAA 412
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                                                                           Length 204652;
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                                                                    Score 54.8; DB 2; Length 2
Pred. No. 0.069;
0; Mismatches 142; Indels
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Arabidopsis thaliana DNA chromosome 4, BAC clone
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                                                                                                        Matches 153; Conservative
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                                                                                       Similarity
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                                                                    Query Match
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VERSION
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JOURNAL
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LOCUS
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Arabidopsis thaliana DNA chromosome 4, contig fragment No. 64.
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Rose, M., Hempel, S., Entian, K.-D., Mewes, H.W., Lemcke, K. and
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Lemcke,K. and Mayer,K.F.X.
Unpublished
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                                                                                                                                                                                                                                                                                                                                Length 89904;
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                                                                                                                                                                                                                                                                                                                                      4.1%; Score 54; DB 8;
56.6%; Pred. No. 0.088;
tive 0; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 56.6
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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KEYWORDS
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obvious genmodel"
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us-09-905-558c-3.rge

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              strong similarity to gene PR-1 protein - Medicago cula, PIR2:S47171
                               truncatula, PIR2:S47171
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signatures Aal47-157; Extracellular proteins
SCP/Tpx-1/Ag5/PR-1/Sc7 signatures AA173-184
contains EST gb:225548, AA586201, AA712838, AA712715"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at@tigr.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1409. .115321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Address all correspondence to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana chromosome II section 91 of 255 of the complete sequence. Sequence from clones F26H6, F9013, F19G14. AC006248 AE002093
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bobermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 11522)
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Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 AAATTAAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAA 378
                                                                                                                                                                                                                                                                                                                                                                                    379 CAACTITACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACATAGTCTA 438
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8
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0.11;
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                                                                                                                                                                               14761. .14921
                                                                                                                                                                                                                                                                                                              4.18;
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                                                                                                                                                                                                                                                                                                                                Local Similarity
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Matches 120;
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PUBMED
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AUTHORS
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JOURNAL
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overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at.html).
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prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Mashington), Genscan (Chris Burge, Mashington), Genscan (Chris Burge, Mashington), Genscan (Chris Burge, Mathington), Genscan (Chris Burge, Manotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Proteins. Genes encoding tRNAs are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSNIKDITSLNSKMGHFNFFSVHHFNITGVTITAPGDSPNTDGIKMGSCSNIQISDIN
IGTGDDCIAILSGTTNLNISNVNCGPGHGISVGSLGKSKDEKDVKDLIVEDVIENGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGIRIKTWESSASKIIVSNEVYENIQMIDVGKPINIDQKYCPHPPCEHERKGESHVQI
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Rattus norvegicus clone CH230-236F15, WORKING DRAFT SEQUENCE, 50
unordered pieces.
AC105576.1 GI:18092798
HTGS. HTGS. PHASEI; HTGS_DRAFT.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8079 IGATIAITGIAAIAGIAAICAAAAAGGIGAAITAAIAGIAITIAACAIAAIAAITAGIAA 8020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 ATCATCACATATATCACAATATTTTCTAAATTAAAATTAAAACTAAAAATGACTAAAATTT 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53.8; DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.1;
14667. .>14757)
/gene="At2g15500"
<13713. .>14757
/gene="At2g15500"
/note="F9013.5"
                                                                                                                                                                                                                                                                                          /codon_start=]
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Rattus norvegicus
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JOIN (~11828 . . 12737, 12932 . . . > 13404)
                                                                                                                                                                                                                                                                                                                                                  /translation-"MACISFAFKALCFCLFFIVVASRSTVRFKVFNVQRHGAKPDGKT
DANNARFRISMSRACKRISGSSKIYVPGTFVLGGVEFVGLCKNPIEFIIDGTLLAPAN
PSDIKQDTWINFRY THNLSYSGSSTLDGGGKGSWPHNDCHNNPECITOGTLAPAN
NSNIKDITSLNSKMGHFNFFSVHHFNITGVTITAPGDSPNTDGIKMGSCSNIQISDTN
NGTGDDCLAILGGTTWLNSNVNCGPGFGFGSVGSKNEREKGARDLYRFNVTFTAF
DGTRANCAILLSGTTWLNSNVNCGPGHGISVGSGKNKDRSKCARDLYRFNVTFTAFTS
DGTRATTWESSASKILTVSNRYVENIQMIDVGKPINLDOKYCPHPPCEHERKGHYQIQ
LKKLKNIYGTSKNKVAMNLQCSKIFPCKNVELIDINIKQNGVKDGSSTSVCENVDGFAR
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VILLDHKAATGGFVTHGGWNSTLEGIAAGLEWYTWPKGAEQFYNEKLLIKVLRIGVNVG
YELLVKKGKLISRAQVEKAVREVIGGEKAEERRLRAKELGEWAKAAVEEGGSSYNDVN
KFMEELNGRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VADMFFPWATESAEKIGVPRLVFHGTSSFALCCSYNMRIHKPHKKVASSSTPFVIPGL
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                                                                                                           join(4336. .4479,4682. .4993,5202. .5726,5830. .6057)
/gene="AL2g15470"
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/protein_id="AAD17393.1"
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                                                                                                                                                                                                                                             /product="putative polygalacturonase"
/protein_id="AAD17391.1"
/db_xref="G1:4335713"
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/gene="At2g15490"
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/gene="At2915480"
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/rpt_family="(TAA)"
complement(8080..8183)
/rpt_family="(GAAAA)"
complement(8739..8780)
/rpt_family="(CAAAA)"
join(~8823..9813,9995..>
/gene="At2915480"
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complement(7735. 7838)
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/rpt_family="(TAAAA)n"
7220, .7281
/rpt_family="(TA)n"
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/note="F9013.3"
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Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hartis, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hornandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Varlsson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Luda, Kovar, C., Karlsson, E., Kelly, S., Khan, V., Keal, B., Lewis, L. C., Louiseged, H., Lozado, W. Lu, X., Ludar, N., Lewis, L., Lu, J., Lu, S., Ludar, M., Martinez, E., Massey, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nuyen, A., Nuyen, N., Nuyen, R., Pace, M., Payton, B., Peery, J., Perters, L., Pickens, R., Pane, M., Payton, B., Peery, J., Petters, L., Pickens, R., Pane, M., Payton, B., Peery, J., Petters, L., Pickens, R., Pane, M., Savety, G., Scherer, S., Scott, G., Shen, H., Stonek, H., Stuton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tang, H., Wall, K., Walliams, G., Walliams, 
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NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 190296 bases at least Q30
Consensus quality: 194221 bases at least Q20
Estimated insert size: 190368; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 3.5x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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16432: 9
26891: 9
26991: 9
39114: 9
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Direct Submission
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Chen, Y., Giles, K.L., Payton, M. E. and Greenstone, M. H.
Identifying key cereal aphid predators by molecular gut analysis
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Chen,Y., Giles,K.L., Payton,M.E. and Greenstone,M.H.
Direct Submission
Submitted (10.APR-2000) Entomology and Plant Pathology, Oklahoma
State University, 127/110 Noble Research Center, Stillwater, OK
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Mitochondrion Rhopalosiphum maidis
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Pterygota; Neoptera; Parancoptera; Hemiptera; Sternorrhyncha;
Aphidiformes; Aphididea; Aphididae; Aphidini; Rhopalosiphum.
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/db_xref="taxon:10116"
/clone="CH230-236F15"
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                                         maidis"
                1. .614
/organism="Rhopalosiphum ma
/organelle="mitochondrion"
/db_xref="taxon:43146"
<1. .>614
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Plasmodium falcipa
                                                                            7, 2002, 07:29:53; Search time 166.564 Seconds (without alignments) 13503.300 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                               **Control of the control of the cont
                                                                                                                                        1310
1 cccatcgctgctttgtctac......caagggaaagtgatcggatg 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                       Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 1736436 segs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
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AAF81468
AAS45444
ABL32458
ABL34124
ABL34241
AAZ17263
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_032802:*
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Maximum DB seq length: 200000000
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                                                                                                                       This is the nucleotide sequence of the 5' untranslated region of the novel corn fad2-2 gene that codes for delta-12 desaturase (see AAY32344). The invention generally relates to the preparation and use of nucleic acid fragments comprising all, or substantially all, of a corn oteosin promerer (see AA235165-77), a stearcy1-ACP desaturase (see AA235199-80) and a delta-12 desaturase, which can be used individually or in combination to modify the lipid profile of corn. Suppression of delta-12 desaturase expression can increase the oleic acid content of the seed oil. Also claimed are seeds of such plants, oil obtained from the grain of such plants, animal feed, use of the oil in food, feed, and cooking oil or industrial applications. The promoter region of fad2-2 may be used to express a gene of interest in transgenic corn plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                         3444 TCGCGTGATCGTCCACACGCTTGCTGTCGTCGCCTACCCAAGTTGACGCGTGCTGCTT 3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3504 CTTCTTCCCGGCGACCGTTCGAGGGACTGCACTGCGTACACCTTCCTGCACCTGCGACTTCGT 3563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3564 ACGACTACATCGAACAACAACACGAGATGTCTCGTGTGAATGGAGCCACTGGTGCCTTGA 3623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATCGGTCCCTCCGCTGGGTACACTCTGTTCTTCGTATTTGTGCAT-GTTTCATTGCTG 3682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New maize oleosin promoter, used for producing transgenic plants with altered fatty acid composition of the oil, used e.g. in animal feeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 CTTATTCA-GACTACCGTTCGAGTGACTGCATGGCGTACATCTTTCTGCATCGACTTTGT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ACGCCTACATCGAACATATACACGAGATGTCTCGTGTGAATAGAGTCACTAATGCCTTAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 5 TCGCTGCTTTGTCTACATCATGTTCTTCATCATCCTCCCCAGGCGACGCGTGCTGCTTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corn; male reproductive tissue; plant regulatory sequence; Zea mays; promoter; transcription regulation; operably linked gene; monocot; dicot; wheat anther; plant fertility; insect tolerance; pathogen tolerance; herbicide tolerance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3743 CTGATTTTCTGGATTAAATTAAAACTAAAAATGCCTAACTTTCTAACACGTCCGA 3797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 ATATTTTCTAAATTAAATTAAAACTAAAAATGACTAAATTTCTAACACCAACGA 358
                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                        Length 12313;
                                                                                                                                                                                                                                                                                                                             Sequence 12313 BP; 2845 A; 2969 C; 3170 G; 3329 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      60; Indels
                                                                                                                                                                                                                                                                                                                                                        Score 235; DB 21;
Pred. No. 3.3e-50;
0; Mismatches 60;
                                                                                                Example 2; Page 80-84; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS96571 standard; DNA; 2126
                                                                                                                                                                                                                                                                                                                                                        17.9%;
82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corn promoter sequence #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   Matches 293; Conservative
                          WPI; 2000-097535/08.
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200183790-A2.
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 Shen JB;
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The present invention relates to the isolation of plant regulatory sequences from the male reproductive tissues of corn (Zea mays). The promoter sequences, fragments, regions or cis elements of the sequences, capable of regulating transcription of an operably linked DNA sequence. The promoter sequences confer enhanced expression of operably linked genes in monocot or dicot male reproductive tissues, such as an thers, especially wheat anthers and is useful for regulating transcription of a DNA sequence, by operably linking the DNA sequence. The promoter sequences are useful in plants to regulate transcription of target genes including genes for control of fertility, insect or pathogen tolerance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation experiments. The promoter sequences can be used in hybridisation assays of other plant tissues to identify closely related or homologous genes and associated regulatory sequences. AASSPSSB-AASSPSST represent the
                                                                                                                                                                                                                                                                                                                           Novel promoters isolated from corn for controlling gene expression in male reproductive tissues, such as anthers, tassels, and to regulate transcription of target genes including genes for insect or pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 CITATICA-GACTACCGIICGAGIGACIGCAIGGCGIACAICTITCIGCAICGACIIIGI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TCGCTGCTTTGTCTACATCATGTTCTTCATCATCCTCCCCAGGCGACGCGTGCTGCTGTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24; Length 2126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%; Score 232.8; DB 24; Length 83.0%; Pred. No. 5.6e-50; tive 0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 ATATTTTCTAAATTAAATTAAAACTAAAATGACTAAATTTCTAACA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 CTGATTATCTGGATTAAATTAAAACTAAAAATGCCTAACTTTCTAACA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2126 BP; 607 A; 419 C; 433 G; 667 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corn promoter sequences of the present invention.
                                                                                                                                                                                                  Masucci JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 115-116; 121pp; English.
                                                                                                                                                                                                     Malven M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF81468/c
ID AAF81468 standard; DNA; 1888 BP.
30-APR-2001; 2001WO-US13739
                                                                 01-MAY-2000; 2000US-201255P.
                                                                                                                                   (MONS ) MONSANTO TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 289; Conservative
                                                                                                                                                                                                     Dubois P,
                                                                                                                                                                                                                                                                WPI; 2002-055481/07.
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us-09-905-558c-3.rng

(first entry)

18-DEC-2001

AAS4544;

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The present invention relates to novel corn promoter sequences (see expression of a second polynucleotide molecule in a transgent plant tissue. In addition, the promoter sequences are useful for providing plants with herbicide resistance. The promoter sequences are useful for providing plants with herbicide resistance. The promoter sequences are suitable for selectively modulating expression of any operatively linked gene and provide additional regulatory element diversity in a plant expression vector in gene stacking approaches. The present sequence is one such corn promoter sequence is one such corn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heterologous gene expression in plants, comprising regulatory sequences located upstream to plant DNA structural coding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGTTCGAGTGACTGCATGGGCGTACATCTTTCTGCATCGACTTTGTACGGCTACATCGAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  724 CATACACACGAGATGTCTTGTGTGAATTGGGCCGCTGATACTTTGAGCATCGGTCCCTTC 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATATACACGAGATGTCTCGTGTGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 GTAGGGTACATTCTGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTACTGATTATAC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter nucleic acid sequences useful for regulating
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0; Mismatches 114; Indels
                                                                                                                 Corn; promoter; transgenic plant; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - Sequence 1888 BP; 569 A; 443 C; 423 G; 453 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conner TW;
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63.9%; Pred. No. 4.6
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                                                              Corn promoter clone #700342364
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                                                                                                                                                                                                                                                                                                                                                                                                       99US-0154182
     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MONS ) MONSANTO CO.
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                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1999;
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     08-JUN-2001
                                                                                                                                                                                                                                                                                         22-MAR-2001
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hes 227;
                                                                                                                                                                          Zea mays.
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Matches
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AAS45444 standard; DNA; 6327

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Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, arthritis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                               Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2657 TATTGTTGATAGTTTGGATTTTTTTAGGTTTTTGTTTTATATATATATATATA 2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTATACA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arterlosclerosis comprising fragments of chemically modified genes associated with cell cycle -
                                                                Chemically pretreated genomic DNA associated with cell cycle #75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6327 BP; 1833 A; 93 C; 1407 G; 2994 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.8%; Score 50.2; DB 22;
60.7%; Pred. No. 0.013;
ive 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 149; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin
                                                                                                                                                                                                                                                                                                                                               15-MAR-2000; 2000DE-1013847.
06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                 15-MAR-2001; 2001WO-EP02945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | || || || || || || || 2777 TATAAATAAAGTT 2791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-602751/68.
                                                                                                                                                                                                                                               WO200168911-A2.
                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                  20-SEP-2001
                                                                                                                                                                                  PCR primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1416 TTAATCAAAATACTCTAAACTCAACTCAACAATAAAAACTACATATCTATATACA 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TACATIGIICTATITCGAATITCACICIATAAACAACATAGICTACAAIGGAAAACA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 ITAITIGIGCATAITITIATIGITGITGTITACIGATIATACGAGIAGITATACATACATGCA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 CATACATATCATCACATATATCACAATATTTTTTTTAAATTAAAATTAAAACTAAAAATGAC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTC-----
                                                                                                                                                                antiarteriosclerotic; antianaemic; oytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiathritic; antidiabetic; antiporiatic; antiinflammatory; cancer; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10133 BP; 3075 A; 70 C; 2051 G; 4937 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 431; 32pp + Sequence Listing; German.
                                                                                                                 Human immune system associated gene SEQ ID NO: 431.
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            ABL32458 standard; DNA; 10133 BP.
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51.0%;
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2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP07537
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 51.0 Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2002.
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                                                 ABL32458;
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ABL32458/
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute mysloid leukaemia, Alzheinmer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 ICICCAACAACITIACCIAITCIACATIGITCIAITICGAAITICACICIAIAAACAACA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antilnflammatory; cancer: eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 CTAAATTAAAATTAAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.8%; Score 49.4; DB 24; Length 73334;
53.3%; Pred. No. 0.06;
Live 0; Mismatches 91; Indels 0;
                    Sequence 73334 BP; 18968 A; 858 C; 15329 G; 38179 T; 0 other;
451 GIGCTTTGTACGACTATATACGCGATGTGTGGCCTACAACATAAAAAAATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2097; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO: 2097.
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                                                                                                                          ABL34124 standard; DNA; 73334 BP
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2000DE-1043826.
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.8
Best Local Similarity 53.3
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytosine methylation
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-1999;
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24-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                         AA217263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of human immune system associated
genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, ansemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 TGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCCGTAGGGTACATTCTGTTCTTCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 TATTIGIGCATATITITATIGITGTTTACTGATTATACGAGTAGTTATACATACATACACAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 ATACATATCATCACATATATCACAATATTTTTTTTAAATTAAATTAAAACTAAAAATGACT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; encroprotective; anti-HIV; anticonvulsant; ophthalmological; antitheumatic; antiarthritic; antidiabetic; antipsoriatic; antinfiammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; theumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 2214; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11691 BP; 3695 A; 49 C; 1861 G; 6086 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 2214.
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3.8%; Score 49.2;
Best Local Similarity 51.1%; Pred. No. 0.
Matches 140; Conservative 0; Mismatche
                                                                                                                                                                     ABL3421/C
XX
ABL34241/C
XX
ABL34241;
XX
ABL34241;
XX
ABL34241;
XX
To-MAR-2002 (first entry)
E Human immune system associated gene
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Human; immune system disease; cytosiantiarterioscierctic; antianaemic; concurrence for antiarterioscierctic; antianaemic; concurrence for antiarterioscierctic; antianaemic; concurrence for antiarthritic; antidiarterioscov
XX
AD Homo sapiens.
XX
AD-JUN-2002.
XX
AD-JUN-2001; 2001WO-EP07537.
XX
AD-JUN-2001 AD-J
                                                                                         59055 TCATCTATCATAA 59041
                                           432 TAGTCTACAATGGAA 446
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The present invention describes a library of human polynucleotides

C comprising the sequences given in AA21253 to AA21779. Also described is

a method of detecting differentially expressed genes correlated with the

cancerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

suspected of being cancerous, where the gene product is encoded by one

of the 5248 polynucleotide sequences given in AA212532 to AA21779. The

of the 5248 polynucleotide sequences given in AA212532 to AA21779. The

of the 5248 polynucleotides can be used as a source of primers and probes, which can

c polynucleotides can be used as a source of primers and probes, which can

c mapping, tissue typing or profiling, forensics, genetic analysis and

detection of polynorphisms. Polypeptides encoded by the polynucleotides

can be used for raising antibodies for experimental, diagnostic and

therapeutic purposes. The polynucleotides may also be used to construct

arrays for diagnostics (which may be used to determine function of an

encoded protein); and to detect differences in expression levels between

two cells (e.g. to identify abnormal or diseased tissue in a human, to

identify a genetic predisposition or susceptibility to a disease such as
340 AAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene expression product cDNA sequence SEQ ID NO:4735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, García PD, García V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo E, Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lamson G, Leshkowitz D, Pot D, Randazzo F, Re
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                   6699 TTTCAAAATAATTTACACAATAAAAAAAATACA 6666
                                                                                                                                                                                                                                                                                         GTTCTATTTCGAATTTCACTCTATAAACAACATA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 2250-2251; 2479pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ17263 standard; cDNA; 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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WPI; 2001-607531/69.
                                                                             Query Match
Best Local Similarity
Matches 147; Conserva
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                                                                                                                                                                                                                                                                                                              TTTAAATTATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2000;
19-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                          AAS56505;
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                                                                                                                                                                                                                                                                                              208
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diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                    995 CACCCTGTCGGCCCTTTGTTTATTCATCCCGAAATCTCATCTGCCCCCACGGCCGACTGC 1054
                                                                                                                                                                                                                                                                    CCCGTGCCCACTCCACGTCCACGGCACCATCCCTCTGCAGCCGCTCACCAGCCATGCC 874
                                                                                                                                                             935 CGTGTCGGTCCGCGTCGGCAACGAGGCGGCCCGCGCTGCTGAGTCCCCTGGACACCCGA 994
                                                                                                                                                                                                                                  755 CACTACCCCAACCTCTCACCGAAAAACCGCGCTGGATCGGCAAATCAAACGAGGTGGTGC 814
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated human polynucleotide (AAH75398)
                                                                                                                                                                              875 GIGICGCGGAACGCCACAACCACCCCCAACCCACICACGAAACCCCGTCCCGGCCGTGCC
                                                                                        ;
0
                                                                       DB 20; Length 1337;
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; antisense-therapy; gene-therapy; diagnostic; forensic; gene mapping; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostics,
                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum MAL3P8 polynucleotide SEQ ID NO 16
                                                                                        Indels
                                                     Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
                                                                     Score 48.8; DB 20;
Pred. No. 0.015;
); Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide for treatment of diseases, antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 106; 135pp; English.
                                                                 3.7%; Scor
32.4%; Pred
                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RT;
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                    AAH93294 standard; DNA; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-2000; 2000WO-US35190
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac
                                                                                 Best Local Similarity 32.4
Matches 101; Conservative
                                                                                                                                                                                                                                                                                        1055 GCTGCGCCGCCC 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
                                                                                                                                                                                                                                                                                                    650 CCCCCCCCC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-451890/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C,
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                                                                          Query Match
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encoding a novel polypeptide (AAG64527) useful in antisense-therapy and gene-therapy, in diagnostics, forensics, gene mapping and identification of mutations responsible for genetic disorders and other traits. Polynucleotide sequences with potential homology were also identified (AAH93283-AAH93385).
                                                                                                                                                                                                                                                                                   208 ITCTGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTAT 267
                                                                                                                                                                                                                                                                                                                                                                                                           328 CTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTAC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 CTATICTACATICITCTATITCGAATITCACTCTATAAACAACATAGICTACAATGGAAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGTGCTTTGTACGACTATATACGCGATGTGTGGCTACAAAATAAAAAATATAGTCGT 507
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 222 polypeptides associated with ovarian and endometrial cancers, useful for diagnosing, preventing and treating cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; ovarian cancer protein; cancer; tumour; ovarian cancer; endometrial cancer; cytostatic.
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0
                                                                                                                                                                                       Score 48; DB 22; Length 399;
pred. No. 0.014;
0; Mismatches 165; Indels
                                                                                                                                             Sequence 399 BP; 225 A; 24 C; 15 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA for an ovarian cancer protein #129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505/c
AAS56505 standard; cDNA; 326
                                                                                                                                                                                              3.7%;
ilarity 47.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2001; 2001WO-US09062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000; 2000US-190710P.
22-JUN-2000; 2000US-213748P.
19-DEC-2000; 2000US-257276P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGAAGATTGAA 519
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01-SEP-2000; 2000DE-1043826.

(EPIG-) EPIGENOMICS

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The invention relates to human polynucleotides encoding proteins

The invention relates to human polynucleotides encoding proteins

Expected with ovarian and endometrial cancers. The polynucleotides and

the proteins they encode may be used in the prevention, diagnosis and

treatment of diseases associated with the inappropriate expression of

covarian and endometrial cancer polypeptides (OECPS). For example, the

polynucleotide (or an expression vector comprising the polynucleotide)

cand the OECP may be used to treat disorders associated with decreased

and the OECP may be used to treat disorders associated with decreased

can fifet the activity of OECPs by expressing inactive proteins or to

supplement the patients own production of them. Additionally, the

couplynucleotide may be used to produce the OECPs, by inserting the nucleic

polynucleotide and its complementary sequences may also be used as DNA

couplement incleded and its complementary sequences may also be used as antigens in

couple of restorative therapy. The OECPs may also be used as antigens in

the production of anti-OECP antibodies and in assays to identify

antagonists may also be used to down requilate expression and activity.

The anti-OECP antibodies may also be used as diagnostic agents for

the production the presence of OECP in samples (e.g. by enzyme linked

immunosorbant assay (ELISA)) and hence diagnose patients with

contracting the present sequence is a ovarian and endometrial cancer linked

contraction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 TGTTCTTCTTATTTGTGCATATTTTTATTGTTTACTGATTATACGAGTAGTTATACA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 TITITITITITITITITITITITICAGGATIGAACACATITITIAATIATIAGAAATACA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 TACATGCATATAATTAACCTTTAATTTATTAAAAAAAATTATGGTCATGAAAACA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antishemmatic; antiarthritic; antidabetic; antipsoriatic; antiloflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilopsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 47.8; DB 22; Length 326;
55.0%; Pred. No. 0.014;
.1ve 0; Mismatches 77; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 AAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 2098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 326 BP; 130 A; 48 C; 34 G; 114 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL34125 standard; DNA; 73334 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000DE-1032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 94; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 ACATATATCACAATATTTTTCTAAATTAAAACTAAAAATGACTAAATTTCTAACA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilopsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 CCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATTGTTCTATTTCGA
                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, usr for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 73334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 73334 BP; 24605 A; 858 C; 14432 G; 33439 T; 0 other;
                                                                                                                                                                                                       Claim 1; SEQ ID NO 2098; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%; Score 47.8; DB 24;
11.1%; Pred. No. 0.16;
Ve 0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 ATTTCACTCTATAAACAACATAGTCTACAATGGAAAACA 450
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ID ABL33574 standard; DNA; 6627 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 51.1%;
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                  Piepenbrock C,
                                                                                                     WPI; 2002-130909/17
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Venter JC;

Gardner M,

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98US-0107131 99WO-US26796

HOFFMAN S. CARUCCI D. GARDNER M.

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Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection
                                                                                                                                                                                                                                  Disclosure; Page 493-495; 577pp; English.
                                                                                                                             Hoffman S, Carucci
                                                                                                                                                     WPI; 2000-365347/31
                                                                                                   (VENT/) VENTER J C.
         05-NOV-1999;
                                  05-NOV-1998;
                                                            (HOFF/)
(CARU/)
                                                                                      (GARD/)
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                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                              The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid theumant Alzheimer's disease, ADIS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6331
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                                                                                                                                                                                                                                                                                                                                                                                                                        6510 TACTCTTTAAAATACCTACTAATTCTCAATTCCTTTCATCCTAACATTAACCTAAATAA 6451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
                                                                                                                                                                                                                                                                                                                                                                                               - 192 TACTCCGTAGGGTACATTCTGTTCTTCTTATTTGTGCATATTTTTATTGTGTTGTTTACTGA 251
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6390 CTAACTITACCCAACTAAAAAATAAAAAACTAAAATITAAACCCAAAAAACTAAAACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 TTATACGAGTAGTTATACATACATGCACATACATATCATCACATATATCACAAATATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 GTTTTCTCCAACAACTTTACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 AACATAGTCTACAATGGAAAACAGTGCTTTGTACGACTATATACGCGATGTGGGCTACA
                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                            DB 24; Length 6627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome 2; human malaria parasite; protozoacide; infection; insecticide;
                                                                                                                                                                                                                                                                                                                                            Score 47.4; DB 24; Length Pred. No. 0.069; O; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 6627 BP; 2052 A; 117 C; 1386 G; 3072 T; 0 other;
                                                                                                                                                                       Claim 1; SEQ ID NO 1547; 32pp + Sequence Listing; German
                                                                  Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA70152 standard; DNA; 6033 BP
                                                                                                                                                                                                                                                                                                                                            Query Match 3.6%;
Best Local Similarity 49.2%;
Matches 155; Conservative (
30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826.
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                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antimalarial; malaria;
                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum
                                                                                                                                               cytosine methylation
                                                                                         WPI; 2002-130909/17
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                                                                  olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum.

Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

CC (I) and (II) are useful for the development of vaccines against

CC (I) and infection. (I) and polycional antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in consequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasite in parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and mosquito drugs. AAA70078 to AAA70287 and AABB1814 to AAB18352 represent nucleotide and protein sequences given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2403 TTTTGAAAATTCATTCAATATATATTTCATATAAATTGAAAGATATTATACACATTCCA 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 TACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACATAGTCTACAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2463 СТТАВАТСТАТТАТСАВТЯТТТСАВСЯТТТТЯТТЯВАВАТТТВАВТТТВАВАВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47.2; DB 21; Length 6033;
Pred. No. 0.074;
0; Mismatches 123; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6033 BP; 3019 A; 437 C; 707 G; 1870 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL16482 standard; cDNA; 281 BP
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Matches 121; Conservative
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18 bases of a chemically pretreated gene associated with gene requiation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or seta/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac althma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preclampsia, graft versus host disease. The present sequence is a sescitated with the human gene regulation associated genes.

Stephen and the sequence data for this specification and is associated with the human gene regulation-associated genes.
Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilatis Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethma: HDR syndrome; congenital heart defect; Saether-Chotzen syndrome; renal disease; Preeclampsia, cardiac allograft vascular disease; colorectal cancer; thyroid cancer; escophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to 224 nucleic acid sequences comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2495 ATAAATATTAAAATAAATTAAATTTCACATTATCTTAATTTACAAAAACTAAATATCTA 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 ATACATATCATCACATATATCACAATATTTTTTTTAAATTAAATTAAAACTAAAAATGACT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 AAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6107 BP; 1822 A; 187 C; 1337 G; 2761 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 46.8; DB 24;
49.2%; Pred. No. 0.094;
live 0; Mismatches 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                            2000DE-1019173.
2000DE-1032529.
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Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                              WO200177375-A2
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human breast cancer expressed polynuclectides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynuclectides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynuclectides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 ACATGCTTATAATTAACCTTAAATTTATTAAAAATAAATTATGGTCATGAAAAACAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 GTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTATACAT 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide useful as a marker for the diagnosis of breast cancer
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Pred. No. 0.024;
0; Mismatches 77; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 TATGGCTTAAAATTGAAATTTCATAGACATGTAATTTTATTCCTAAAAA 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 281 BP; 93 A; 32 C; 39 G; 117 T; 0 other;
                                                                                       Human breast cancer expressed polynucleotide 8939
                                                                                                                               Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%;
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2000US-0192099.
2000US-0193480.
2000US-0205230.
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25-JUL-2000; 2000US-0220534.
                                                                                                                                                                                                                                                                                                                10-JAN-2001; 2001WO-US00798
                                            (first entry)
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nes 93; Conservative
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                                                                                                                                                                                                                           WO200151628-A2
                                                                                                                                                                              Homo sapiens.
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                                            07-DEC-2001
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AAL16482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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US-08-577-483-14
US-09-182-816-22
US-09-471-528-22
US-09-471-528-22
US-09-634-530-22
US-09-634-530-22
US-09-634-530-24
US-08-81-483-7
US-08-81-1094-4
US-08-81-1094-4
US-09-165-264-8
US-09-385-982-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08232463
Petent No. 5670367
CENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 US-07-820-154A-3
US-08-097-554A-3
US-08-480-640A-3
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US-08-488-237A-3
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AuG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENNE/ACOKET NUMBER: 39,72/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)83-4109
                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.9%; Score 51.2;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-232-463-14
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22313-0299
     IMMEDIATE SOURCE
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   Query Match
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Sequence 1, Appli
Sequence 11, Appli
Sequence 4, Appli
Sequence 10, Appli
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Sequence 63, Appli
Sequence 67, Appli
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109, App
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8247.617 Million cell updates/sec
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                                                                                                                       7, 2002, 07:44:03 ; Search time 39.0149 Seconds
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1 cccatcgctgctttgtctac......caagggaaagtgatcggatg 1310
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/FB_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-843-659-1
US-08-843-659-1
US-08-007-119-14
US-09-007-119-14
US-09-007-119-14
US-08-811-994-63
US-08-443-639-7
US-08-973-462-1
US-08-973-462-1
US-08-97-252-96
PCT-US-06-06352-96
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US-07-638-431-1
PCT-US92-00018-1
US-09-004-838-109
US-08-947-823-1
US-08-487-8268-13
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Maximum Match 100%
Listing first 45 summaries
                                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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51952
19124
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Perfect score:
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Similarity
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                            Matches 145;
Query Match
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                Best Local
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                                                                                                   TGCAGCCGCTCACCAGCCATGCCGTGTCGCGGAACGGCACAACCACCCCCAACCCACTCA 911
                                                                                                                                                            CGAAACCCCGTCCCGGCCGTGCCCGTGTCGGTCCGCGCTCGGCAACGAGGCGGCCCGCGC 971
                                           CGGCAAATCAAACGAGGTGGTGCCCCGTGCCCACTCTCCACGTCCACGCCACCATCCCTC 851
                  Gaps
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                Indels
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Patent No. 5876923
GENERAL INFORMATION:
APPLICANT: Leopardi, Rosario
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN TITLE OF SEQUENCES: 2
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
FILLING DATE: 26 UUL-1996
 d. No. 0.00017;
Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                            1152 TGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCA 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    Pred.
   Best Local Similarity 4.3%; Pre-
Matches 17; Conservative 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 512/474-75777
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512/418-3000
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Texas
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COUNTRY:
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APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2693 CGGCCCCGCCCCAGCCCCGGGCCCCCGGGCCGCCGGCCCAGGCCCGCCCGCCCCCG 2752
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                                                                                                                           714 CAGGCICGCIGGCCCCACGGGCGIGCTGCGGCGCACGAAGGGCACTACCCCCAACCTCTCAC 773
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                                                                                                                                                                                                                                                                                                   714 CAGGCTCGCTGGCCCCCACGGGCGTGCTGCACGAAGGGCACTACCCCAACCTCTCAC
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                                                                                                                                                                                 CGAAAAACCGCGCTGGATCGGCAAATCAAACGAGGTGGTGCCCCGTGCCCACTCTCCACG
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Length 4257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.2; DB 4; Length 4
Pred. No. 0.0063;
0; Mismatches 148; Indels
                                             Indels
                                               148;
3.5%; Score 45.2; DB 2;
49.3%; Pred. No. 0.0063;
tive 0; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 1999-03-01
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1996-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09259821A Patent No. 6210926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.5%;
Best Local Similarity 49.3%;
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA; COGANISM: HERPES VIRUS, TYPE US-09-259-821A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 00
PRIOR FILING DATE: 1996-07-:
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
                                               Conservative
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US-08-843-659-1
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NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewicz 6 No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION UNDRER: 36,317
REFERENCE/DOCKET UNDRER: DFCI-0029
TELECOMMUNICATION INFORMATION:
TELEFRAN: (215) 568-3100
TELEFRAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12001 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-UUE-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Herpes simplex virus
; STRAIN: Herpes Simplex Virus Type 1
US-08-458-568A-11
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
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US-08-749-522-4/C
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Sequence 11, Application US/08458568A
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       714 CAGGCTCGCTGGCCCCACGGGCGTGCTGCGTGCACGAAGGGCACTACCCCAACCTCTCAC 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         894 CCACCCCCAACCCACTCACGAAACCCCGTCCCGGCCGTGCCCGTCGGTCCGCGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          954 CAA-CGAGGGGGCCGGGGTGCTGAGTCCCCTGGACACCCGACACCCTGTCGGC 1006
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                                                          APPLICANT: Leopard1, Roasrio
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERRES SIMPLEX VIRUS US3 AND ICP4
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOld, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,659
FILING DATE: Concurrently Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:519
TELEPHONE: (512) 474-757
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Sequence 1, Application US/08843659
Patent No. 6218103
                                                                                                                                                                                                                                                                            United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 49.33
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                        COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
US-08-843-659-1
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714 CAGGCTCGCTGGCCCCACGGGCGTGCTGCGTGCACGAAGGGCACTACCCCAACCTCTCAC 773
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                                                   Gaps
                                                                                                                                                                                                                                                                                834 TCCACGGCACCATCCCTCTGCAGCCGCTCACCAGCCATGCCGTGTCGCGGAACGGCACAA
                                                                                                                                                                                                                                                                                                                                                                           894 CCACCCCCAACCCACTCACGAAACCCCGGCCGTGCCCGTGTCGGTCCGCGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              954 CAA-CGAGGCGGCCCGCGTGCTGAGTCCCTGGACACCCGACACCCTGTCGGC 1006
                                                   ij
Query Match 3.5%; Score 45.2; DB 1; Length 12001; Best Local Similarity 49.3%; Pred. No. 0.011; Matches 145; Conservative 0; Mismatches 148; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08749522
Patent No. 6096950
GENERAL INFORMATION:
APPLICANT: John, Maliyakal
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                      LOCATION:
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                                                                                                                                                                                                                                                                                                                                LOCATION:
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Sequence 14, Application US/09007119C

Patent No. 6300541

GENERAL INFORMATION:

APPLICANT: Lighfoot, David A.

APPLICANT: Marken, Khalid

TITLE OF INVENTION: Soybean Cyst Nematode Resistant Soybeans,

TITLE OF INVENTION: Soybean Cyst Nematode Resistant Soybeans and Methods of

TITLE OF INVENTION: Breeding and Identifying Resistant Plants

FILE REPRENEE: Sou Illinois 1268/2 Sequence Listing

Patent No. 6300541

CORRENT APPLICATION NUMBER: US/09/007,119C

CORRENT FILING DATE: 1998-01-14

EARLIER PAPLICATION NUMBER: 60/035,335

EARLIER PILING DATE: 1997-01-14

NUMBER OF SEQ ID NOS: 20
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                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,522
      FIBER-SPECIFIC PROMOTERS
                                                                                                                                                                                                                                                                                                                                    APPLICALON
FILLING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 670513.90244
TELEPHONE: (414) 277-5709
TELEPHONE: (414) 277-5709
TELEPRAX: (414) 277-5709
TELEPRAX: (414) 277-3552
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2781 base pairs
                                                                SSEE: Quarles & Brady
F: 411 East Wisconsin Avenue
Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1163 TTTAATTTATTTTATATATCATAT 1139
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EDNESS: double
                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                   CORRESPONDENCE ADDRESS
        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                           STREET:
CITY: Mi
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221 ATTIGIGCATATITITATIGITGTITACIGATTATACGAGTAGTIATACATACATGCACA 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 TACATATCATCACATATATCACAATATTTTTTTTAAATTAAATTAAAACTAAAAATGACTA 340
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OTHER INFORMATION: (a or c or g or t/u)
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; OTHER INFORMATION: (a or c or g or t/u)
US-09-007-119-14
                                                                                                                                                                                                                                                                                                                                            t/n)
                                                                                     LOCATION: (3) OTHER INFORMATION: (a or c or g or t/u)
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                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (610)
OTHER INFORMATION: (a or c or g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (677)..(678)
OTHER INFORMATION: (a or c or g or
                                                                                                                                                                                 OTHER INFORMATION: (a or c or g or
                                                                                                                                                                                                                                                                 or
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LOCATION: (771)..(772)
OTHER INFORMATION: (a or c or
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OTHER INFORMATION: (a or
                                                                                                                                                                                                                                                                                                                       LOCATION: (479)
OTHER INFORMATION: (a or
                                                                                                                                                                                                                                                                 OTHER INFORMATION: (a or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (677)..(678)
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                                                            NAME/KEY: misc_feature
                                                                                                                                            NAME/KEY: misc_feature
TYPE: DNA ORGANISM: Glycine max
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Gaps

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Indels

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457 ATTIGICAAATTIGGTACTCCCTTIGGACTCGTATATAAGAAAAATAACTAATTICACA 398
                                                                                                                                     281 TACATATCATCACATATATCACAATATTTTTCTAAATTAAATTAAAACTAAAAATGACTA 340
                                                                                                                                                           292 ACATATATCACAATATTTTTCTAAATTAAAATTAAAACTAAAAATGACTAAAATTTCTAACA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.2%; Score 41.8; DB 6; Length 1890;
Best Local Similarity 53.3%; Pred. No. 0.038;
Matches 88; Conservative 0; Mismatches 77; Indels 0
                                                                                                                                                                                                                                                                                                                                                             DANIEL A.

TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES
FOR GENETICALLY ENGINEERING DISEASE RESISTANCE AND OTHER
INDUCIBLE TRAITS IN PLANTS
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/393,301
FILING DATE: 13-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 CCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTAC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5312912-3/c; Patent No. 5312912; APPLICANT: HADWIGER, LEE A.; CHIANG, CHIN C.; HOROVITZ,
                    Pred. No. 0.011;
); Mismatches 70;
                                                                                                                                                                                                           341 AATTTCTAACACCAACGACATTGTAATGTTTCTC 375
                                                                                                                                                                                                                                   Sequence 63, Application US/08821994A
Petent No. 6228643
GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
FILE REFERENCE: PPD 50108
CURRENT FILICATION NUMBER: US/08/821,994A
CURRENT FILICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN VET. 2.1
              Best Local Similarity 54.8%; Pr
Matches 85; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 1890
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                                                                                                                                       APPLICANT: Lightfoot, David A. APPLICANT: Lightfoot, David A. APPLICANT: Glbson, Paul T. APPLICANT: Glbson, Paul T. APPLICANT: Glbson, Rabid TITLE OF INVENTION: Soybean Sudden Death Syndrome Resistant Soybeans, TITLE OF INVENTION: Soybean Cyst Nematode Resistant Soybeans and Methods of TITLE OF INVENTION: Breeding and Identifying Resistant Plants Patent No. 6300541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 809;
268 TATTICTAAAATGICCTICATIGGAACTIGTIAIC 302
                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/007,119C
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,335
EARLIER FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 20
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 809
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                                                RESULT 8
US-09-007-119-10/c
; Sequence 10, Application US/09007119C
; Patent No. 6300541
; GENERAL INFORMATION:
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OTHER INFORMATION: (a or c or
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INFORMATION: (a or
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OTHER INFORMATION: (a or
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LOCATION: (747)
OTHER INFORMATION: (a or
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LOCATION: (795)
OTHER INFORMATION: (a or
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LOCATION: (785)
OTHER INFORMATION: (a or
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NAME/KEY: misc_feature
LOCATION: (1)..(6)
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LOCATION: (506)
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NAME/KEY: misc_feature
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LOCATION: (766)
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NAME/KEY: misc_feature
LOCATION: (797)
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Glycine max
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OTHER INFO
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Score 41; DB 2;
Pred. No. 0.098;
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Patent No. 5705343
GENERAL INFORMATION:
APPLICANT: FEDER, JOHN N.
APPLICANT: FEDER, ANDREAS
APPLICANT: THOMAS, MINSTON J.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: MOLEF, ROGER E.
APPLICANT: MOLEF, ROGER E.
APPLICANT: MOLEF, ROGER E.
APPLICANT: HOWAS, WINSTON J.
APPLICANT: HOWAS, WINSTON J.
APPLICANT: HOWAS, WINSTON J.
APPLICANT: HOWAS, WINSTON J.
APPLICANT: MOLEF, ROGER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08973462B Patent No. 6191270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.1%;
Best Local Similarity 54.3%;
Matches 82; Conservative (
 3.18;
                                      89; Conservative
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   Query Match
Best Local Similarity
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US-08-973-462-1/c
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US-08-599-252-96
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                                                                                                                                                       331 AAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTA 390
                                                                               211 IGITCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTATACA 270
                                                Gaps
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           Length 1441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chappell, Joseph
APPLICANT: Yin, Shaohui
APPLICANT: Tin, Shaohui
APPLICANT: Cornett, Catherine A.G.
TITLE OF INVENTION: Transcriptional Control Sequences and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 13
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                                              Indels
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2259
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,639
FILING DATE: 18-MAY-1995
CLASSIFICATION: 800
ATTORREY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REFERENCE/DOCKET NUMBER: 69-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
INFORMATION FOR SED ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
           Score 41.6; DB 4;
Pred. No. 0.037;
0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08443639
Patent No. 5981843
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
               3.2%;
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                                                Conservative
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EDNESS: double
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MEDIUM TYPE: Floppy
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ADDRESSEE: Greenlee
               Query Match
Best Local Similarity
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US-08-443-639-7
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                                                    Matches 113;
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APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALBARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILLE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILNG DATE: 1998-02-06
EARLIER PILNG DATE: 1998-02-06
EARLIER FILNG DATE: 1995-06-13
EARLIER PILNG DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET: 2.0
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                                                                                                    307 TATATATATATATATATATATATATATTCTATAATTTTCTTTAACTTTTCACAATTTT 248
                                                                            265 TATACATACATGCACATACATCATCACATATATCACAATATTTTTCTAAATTAAATTA 324
                                                                                                                                                         325 AAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTT 384
                                      Gaps
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Length 4254;
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Pred. No. 0.16;
0; Mismatches 69;
                                        80;
                                          0; Mismatches
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Sequence 96, Application PC/TUS9606583
GENERAL INFORMATION:
APPLICANT: BRAYNA, DENNIS T.
APPLICANT: FEDER, JOHN N.
APPLICANT: GYRTRKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: THOMAS, WINSTON J.
TITLE OF INVENTION: METHOD TO DIAGNOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEMOCHROMATOSIS
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                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (((
TELEFAX: 90-4030

INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.18;
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Best Local Similarity 46.48
Matches 122; Conservative
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PCT-US96-06352-96
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                                                                    COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-FEB-1996
CLASSIFICATION: 435
ATTORNEY.AACTION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 96, Application PC/TUS9606352
GENERAL INFORMATION:
APPLICANT: DARANA, DENNIS T.
APPLICANT: FEDER, JOHN N:
APPLICANT: FEDER, JOHN N:
APPLICANT: THOMAS, WINSTON J.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: METHOD TO DIAGNOSE
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                       ATTORNEY/ACENT INPORMATION:
NAME: MURASHIGE, KATE H.
RECISTRAATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-150
TELEX: 90-403
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 ACAGTGCTTTGTACGACTATATA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 TGTGTGATAAATCANANAANANA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.1%;
Best Local Similarity 46.4%;
Matches 122; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-599-252-96
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STRANDEDNESS:
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208 TICTGTICTTCTTATTTGTGCATATTTTTATTGTTTACTGATTATACGAGTAGTTAT 267
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Pred. No. 0.067;
0; Mismatches 141; Indels 0
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06352
FLING DATE:
CLASSITCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,252
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT IRFORMATION:
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REEREROCE/DOCKET NUMBER: 29,959
RELEPRAKE: (202) 887-1500
TELEFPAK: (202) 887-1500
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STATE: DC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US96/06583
FILING DATE:
CLASSIFICATION NUMBER: PCT/US96/06583
FILING DATE:
CLASSIFICATION NUMBER: DS 99,252
FILING DATE:
CLASSIFICATION NUMBER: 29,959
FEFERENCE/COCKET NUMBER: 29,959
FEFERENCE/COCKET NUMBER: 29,959
FEFERENCE/COMPATION INFORMATION:
FELEPHONE: (202) 887-1500
FELEPHONE: (202) 887-15
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7, 2002, 08:30:58; Search time 1237.97 Seconds (without alignments) 14282.232 Million cell updates/sec
                                                                                                      US-09-905-558C-3
1310
1 ccatcgctgctttgtctac.....caagggaaagtgatcggatg 1310
  GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                              13736207 seqs, 6748477542 residues
                                                                                                                                                                                                rotal number of hits satisfying chosen parameters:
                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                November
                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                 Scoring table:
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AL285149 Tetracdon BE455154 HVSMENGOO9 BE455154 HVSMENGOO9 AL071865 Drosophil BH255629 LDH5BAWOO AL071865 Drosophil AL175696 Tetracdon AL108152 Drosophil BM163977 EST56550 AL08704 BDrosophil BM163970 EST56550 AL072804 BDrosophil BM163970 EST56500 AL072804 BDrosophil BL953364 HVSMEWOO1 AL107341 Drosophil BL9263 T22C5-T7 TA AL107313 486093C05 AC104199 QV4-CRN12 AL107313 486093C05 AC104190 BOV4-CRN12 AL10736 BDROSOPHIL BL957313 486093C05 AC104109 GV4-CRN12 AL10736 BDROSOPHIL BC641241 GA EB001 AL106869 BPR LTCGIL BM168596 EST571119

CNS04D0K BR455154 CNS00BK0 CNS00BK0 CNS00BC CNS00BK7 CNS017KF CNS017KF CNS017KF CNS017KF CNS017KF CNS017Z6 BM163973 AZ04630 CNS00HF BM163973 AZ04630 CNS00HF BM163973 CNS00HF CNS00HF

ALIGNMENTS

RESULT

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EST: *

Database

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	DEFINITION	RXL1BAM0001A01r Zea mays L. XLi methyl filtration maize root genomic shotgun library Zea mays genomic clone RXL1BAM0001A01r. DNA
	ACCESSION	sequence, BH255115
	VERSION	BH255115.1 GI:17150008
	SOURCE	GSS. Zea mays.
	ORGANISM	Zea mays
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae: PACC
	REFERENCE	Clade; Panicoideae; Andropogoneae; Zea.
	AUTHORS	Kim,S.W., Yu,Y., Lee,M.C., Yang,T.J., Main,D., Henry,D., Oates.R
		and Wing, R.A.
	TITLE	Genomic shotgun library from maize
	COMMENT	Unpublished (2001) Contact: Wing RA
		Clemson University Genomics Institute
		Clemson University
		100 Jordan Hall, Clemson, SC 29634, USA
		Tel: 864 656 7288
		Fax: 864 656 4293
		Email: rwing@clemson.edu
-		Seq primer: AATTAACCCTCACTAAAGGG
		Class: shotgun
		High quality sequence stop: 374.
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BH255739 LDH5BAM00
AL103998 Drosophil
BH25239 HVSWEM000
AL053013 Drosophil
BC852371 1024034A0
AQ251130 F26H6-Sp6
ALO71298 Drosophil
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ALO71298 Drosophil
BL950718 HYSWEM002
AL106795 Drosophil

AW928053 BI885732 CNO3106X AU087781 CNSO16XK BH255739 CNSO14D0 B1952390 CNSO091P BGB52371 AQ231130 CNSO0FVE CNSO0FVE CNSO0FVE CNSO16IP B1950718

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374 223 496 496 572 1101 500 935 534 1058 818 925 936 798 1101 1101 481 481 848

BH255115 RXLIBAMOO

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_hum: *
em_gss_inv: *
em_gss_pln: *
em_gss_vrt: *

gb_est1:*
gb_est2:*
gb_htc:*

*:ss6_dp

SUMMARIES

В

Query Match Length

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346 CTAACAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAACAC 38
                                                                                                                                          73
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                       Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
AW928053/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                       Matches
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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/RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 17-DEC-2001
                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006023 row: 39
Methyl-filtration library, Nuclei DNA was digested with Sau3Al, size fractionated and transformed to E.Coli.XLIBlue."
                                                                                                                                                                                                                                                                                                  AZ921021 2EL_yl 1006 - RescueMu Grid G 2ea mays genomic, DNA
                                                                                                                                                                                                                       156 CCATTCGAGGGACTACACTGCGTACATTTGCCTGCATCGACTGCATA ---CTAAATCGAA 300
                                                                                                                                                                                                                                                                                                                                                                       239 GCAGGGTACATTATGTTCTTAGTGATTGTGCAT-GTTTTACTGTTGTTTACCGCTATATGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                              258 GAGTAGTTATACATACATGCAC--ATACATATCATCACATATATCACAATATTTTTTTAA 315
                                                                                                                                                                                                   78 CCGTTCGAGTGACTGCATGGCGTACATCTTTCTGCATCGACTTTGTACGGCTACATCGAA 137
                                                                                                                                                                                                                                                                            138 CATATACACGAGATGTCTCGTGTGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCC 197
                                                                                                                                                                                                                                                                                                                                                   198 GTAGGGTACATICIGITCTTCTTATITGTGCATATITITATIGITGTTTATACTGATTATAC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                ;
                                                                                                                            DB 12; Length 374;
                                                                                                                                                                0; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  855 California Ave, Palo Alto, CA 94304, USA TE1: 650 723 2227 Fax: 650 725 8221
                                                                                                                                              4.9e-21;
                                                                       115
                                                                                                                            Score 149.2;
Pred. No. 4.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTAAATTAAAACTAAAAATGACTAAAT 343
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Location/Qualifiers
                                                                       70 9
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                                                                                                                          11.4%;
79.9%;
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Walbot, V.
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                                                                       64 c
                                                                                                                                                Best Local Similarity 79.9
Matches 214; Conservative
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AZ921021.1
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Zea mays
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ORGANISM
                                                                     BASE COUNT
ORIGIN
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for FoscueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cepls were transformed and then screened on LB plates with 36 c 46 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 bp mRNA linear EST 30-MAY-2000
945007D02.Y1 945 - Mixed adult tissues from Walbot lab, same as 707
AW928053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Itassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: ECORI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 496)
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 GAGTCACTAATGCCTTAAGCATCGGTTACTCCGTAGGGTACATTCTGTTCTTTTTTG 225
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Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                  Length 223;
                                                                                                                                                                                                                                                                  Score 123.8; DB 12; Length
Pred. No. 9.5e-16;
0; Mismatches 32; Indels
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
815 California Ave,
Fax: 650 723 227
Fax: 650 725 8221
Email: walbod/estanford.edu
Plate: 945007 row: D column: 02.
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                                                                                                                                                                                                                                                                  9.5%;
al Similarity 82.4%;
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Unpublished (1999)
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: abrafish@watcon.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                         268 ACATACATGCACATACATATCACATATATCACAAATATTTTTCTAAATTAAAA 327
                                                                                                                                                                                                           208 ITCTGTICITCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTAT 267
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Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Febr. 314, 286 1800
                                                            Length 496;
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/sex="mixed"
                                                          DB 9;
                                                       Score 107.6; DB 9
Pred. No. 2.4e-12;
0; Mismatches 39
     124
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/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="4490204"
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre drough of the Drosophila was propered to project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 500)
Watanabe,J., Sasaki,M., Suzuki,Y. and Sugano,S.
FULL.malaria: a database for a full.length enriched cDNA library from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                  1027 ТМТМТИНТМТМТМТИТТТИМТМТНТТИННТТИПМТМТМТИТНТНТМТМТМТИТНТИММ 968
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                                                                                                                                                       1. .1101
/organism="prosophila melanogaster"
/plasmid="plealoabC11"
/db_xref="taxon:7227"
/clone_lib="brosBAC"
/clone="BACN03K20"
                                                                                                                                                                                                                                                              501
                                                                                                                                                                                                                                                                                                                                      184;
                                                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                         th 4.4%; Score 58.2; DB : Similarity 19.2%; Pred. No. 0.049; 87; Conservative 182; Mismatches 18
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J35 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Contact: Junichi Watanabe
Institute of Medical Science
Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
The! 81-3-5449-5378
Fax: 81-3-5449-5410
Bmail: jwatanabémanage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo.Nakagawa,R., Maruyama,R., Suyama,A. and Sugano
Suzuki,Y., Yoshitoman characterization of a full length-enriched and
a 5'-end-enriched CDNA library Gene 200 (1-2), 149-156 (1997).
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Submitted (02-70N-1999) Genoscope - Centre National de Sequencage : Spanitted (02-70N-1999) Genoscope - Centre National de Sequencage : Spanitted (02-70N-1999) Genoscope - Centre National : segref@genoscope - Cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - The BDC this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDCP). The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 TATITGEGCATATITITATIGITGITTACCGATIATACGAGIAGITATACATACATGCAC 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 ATACATATCATCACATATATCACAATATTTTTCTAAATTAAATTAAAACTAAAATGACT
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sugano Malaria cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Plasmodium falciparum"
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Pred. No. 0.058;
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25 c 33 g 203 t
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/clone="XPFn5810"
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genomic shotgun library Zea mays genomic clone LDH5BAM0003C03f, DNA
Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 534)
Kim, S.W., Yu, Y., Lee, M.C., Yang, T.J., Main, D., Henry, D., Oates, R. and Wing, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                       921 SGSSGCGSGGSGGSGCCCSGSGCCSSCSSSSSCCCSSCGCCSC 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                      864 CCAGCCATGCCGTGTCGCGGAACGGCACAACCCCCCAACCCACTCACGAAACCCCGTC 923
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                                                                                                                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone="BaCRI4N09"
                                                                                                                                                                                                                                                                                                                       ; Score 57.4; DB 12;
; Pred. No. 0.072;
86; Mismatches 180;
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Unpublished (2001)
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RAGSGKMGSAGSSGRCGGACS 541
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Matches 115; Conservative
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BH255739
BH255739.1
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/organism="Zea mays"
/strain="B73"
/db_xref="taxon:4577"
/dlone="LubshaM000303f"
/clone="LubshaM000303f"
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/lab_host="DH5alpha"
/lab_host="Pdector: pCUGIblu-1; Site_1: Sau3A1; Site_2: Sau3A1;
Methyl-filtration library, Nuclei DNA was digested with Sau3A1, size fractionated and transformed to
E.Coli. DH5alpha."
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.ut...this Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 TICAGITITITICIACIATCAIGAGAATAATATIGIATGITIGITACIATITAGAGIAG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 T----ACACATGCACGTAAATGTCATCACATATTTTATGCAATGTTTTTGGATTAAAT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 TAAGCAATAATTTGCCTAAATTTCTAACACCAACTACATAAGATTTTTCATGTTTAATAC 410
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     SC 29634,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205
                                                                      Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: shotgun
                                                                                                                                               High quality sequence stop: 531.
Location/Qualiflers
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     Clemson,
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Drosophila melanogaster
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100 Jordan Hall, C
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                             shotgun
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7 Triticeae; Hordeum.

1 (bases 1 to 818)

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D., Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected Morex (compatible) seedling
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                                                                                                                                                                                                                                                                                                                     760 HSMTSWMYTTACCMTSMCTSWTSTACCACWCYCTACCAWTATATACTMMTATATHCACTW 819
                                                                                                                                                                                                                                                                                                                                                                                 306 ATTITICTAAATTAAAATTAAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTA 365
                                                                                                                                                                                                                                                        186 ATCGGTTACTCCGTAGGGTACATTCTGTTCTTATTTGTGCATATTTTATTGTTGTT 245
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVSMEm0006C23f Hordeum vulgare green seedling EST library HVCDMAN0014 (Blumeria infected) Hordeum vulgare cDNA clone HVSMEm0006C23f, mRNA sequence.
                                                                                                                                                                                                                        0;
                                                                                                                                                                                            DB 12; Length 1058;
                                                                                                                                             273 others
                                                                                                                                                                                                                          Indels
                                       /organism="Drosophila melanogaster"
/plasmid="pBeloBA111"
/db_xref="Laxon:7227"
/clone_lib="DrosBAC"
/clone="BACN11117"
                                                                                                                                                                                                                        94;
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                          Score 55.6; DB Pred. No. 0.17;
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/organism="Hordeum vulgare"
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/clone="HVSMEm0006C23f"
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              Location/Qualifiers
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                                                                                                                           : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@clemson.edu
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BI952390.1 GI:16296163
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nes 78; Conservative
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Unpublished (2001)
                                                                                                                                             175 c
                                 1. .1058
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pBeloBAC11
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LOCUS
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/note="Vector: pBluescript SK(-); Site_1: ECORI; Site_2: XhOI; Morex (mla) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria gramminis f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-incoulation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value.
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http://www.genome.clemson.edu/projects/Darley. To order

this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)

Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.

(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

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/tissue_type="green seedling leaf"
/lab_host="TJC121"
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Query Match
4.2%;
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Matches 145; Conservative
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AQ251130
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                                                                                                                                                                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr |
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecord digestion of Drosophila DNA provided by the BDGP from the 1809genic strain of Drosophila DNA provided by the BDGP from the 1809genic strain y2; on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              936 bp mRNA linear EST 29-MAY-2001 1024034A05.y2 C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. BG852371 GI:14233555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCACTACCCCAACCTCTCACCGAAAAACCGCGCTGGATCGGCAAATCAAACGAGGTGG 811
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I (bases 1 to 925)
Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/db_xxef="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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                                     Drosophila melanogaster
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Anote-"Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAPP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA MRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRN [5') and XhoI (3') sites,
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                    In Classes 1, U. 3-30, Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Sllflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants: project phase 2 Gene Function and Regulation in Vascular Charles Hauser Contact: Charles Hauser Contact: Charles Hauser Contact: Charles Hauser Down Box 91000

Duke University

Durham, NC 27708-1000

Tel: 919 613 8157

Fax: 919 613 8177

Email: chauser@duke.edu.
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                                                           Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales
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Pred. No. 0.25;
0; Mismatches 133;
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Chlamydomonas reinhardtii. Chlamydomonas reinhardtii
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                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                      Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                                                                                                                                                               Unpublished (1997)
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
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Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
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Pred. No. 0.37;
0; Mismatches 111; Indels
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/organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                        Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seg primer: Sp6
                                                                                                                                                                                                                                                                                                                                                                               /strain="Columbia"
/db_xref="taxon:3702"
/clone="F26H6"
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BAC End Sequences at ATGC
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Arabidopsis thaliana
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Per 191 JUGO BAYE CHEAR FRANCE (E MELL: Sequence December 191 JUGO BAYE CHEAR FRANCE) (E MELL: Sequence Was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Canterted by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp. the same strain used for the BDGP's pl and box to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                         Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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AL106795
AL106795.1 GI:5623841
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731 ATCICTITAYAWATITIYYYYATITCACAATAAWITWCWAAWWIMMAWWIWIAMACMWW 790
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                   Genoscope
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dross BAC) was made by Alain Billaha at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                            7. 481
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/clone="BACN16B22"
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0 a 113 c 142 g 67 t 159 ot
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Conner,T.W., Dubois,P., Malven,M. and Masucci,J.D.
Plant requiatory sequences for selective control of gene expression
Patent: WO 0183790-A 92 08-Nov-2001;
Monsanto Technology LLC (US)
  AX299951 Sequence
AX099709 Sequence
U00989 Zea mays D3
AC108209 Homo sap1
AC090043 Homo sap1
AC090043 Homo sap1
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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AX299951.1 GI:17129442
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AC108209
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        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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318 TAAATTAAAACTAAAAATGACTAAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCA
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/apr
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/gene="Mha1"
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Eukaryotes, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryotes, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneee; Zea.

1 (bases) 1 to 1888)

Anderson, H.M., Chay, C.A., Chen, G. and Conner, T.W.

Plant regulatory sequences for control of gene expression

Patent; WO 0119976-A 65 22-MAR-2001;

MONSANTO COMPANY (US)

MONSANTO COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATATACACGAGATGTCTCGTGTGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCC 197
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                                                      TCGCTGCTTTTGTCTACATCATGTTCTTCATCCTCCCCCAGGCGACGCGTGCTGTT
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Pred. No. 8.4e-19;
0; Mismatches 114; Indels 14;
      Length 2126;
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                               Indels
        DB 6;
      Score 232.8; DB 6
Pred. No. 2.7e-44;
0; Mismatches 57
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AX099709.1 GI:13538763
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/organism="Zea mays"
/db_xref="taxon:4577"
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          17.8%;
83.0%;
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          Query Match 17.89
Best Local Similarity 83.09
Matches 289; Conservative
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/product="H(+)-transporting ATPase" 1203,2316. 2453, join(<1446. 1508,1874. 1993,2105. 2203,2316. 3425,3510. 3629, 2525. 2659,2751. 2593,3010. 3225,3306. 3425,3510. 3629,3722. 3844,3927. 4031,4113. 4257,4379. 4543,4657. 4875,4964. 4996,5091. 5172,5257. 5417,5513. 5689,5768. 5950,
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2525 . .2659,2751 . .2930,3019 . .3225,3306 . .3425,3510 . .3629,
3722 . .3844,3927 . .4031,4113 . .4257,4379 . .4543,4637 . .4875,
4964 . .4996,5091 . .5172,5257 . .5417,5513 . .5689,5768 . .5950,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-MAY-1994) Young-Kwan Jin, Biological Sciences, Purdue University, 339 Hansen Life Science Research Building, West Lafayette, IN 47907, USA
                                                                                                                                                                                                                                                                 ZMU09989

2ea mays D3L H(+)-transporting ATPase (Mha1) gene, complete cds. U09989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea. Zea. Z751 to 2930; 3019 to 3225; 2525 to 2659; Z751 to 2930; 3019 to 3225; 3510 to 3629; 3722 to 3844; 3927 to 3938)
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Jin,Y. and Bennetzen,J.L. Integration of a Plasma Membrane Prafragration and Nonrandom Mutation of Retroelement of Maize Plasse Gene Fragment within the Bsl Retroelement of Maize Plant Cell 6, 1177-1186 (1994)
                                                                                   ACAACTTTACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACAT 432
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3927. :4031 /gene="Mha1" /number=11 4032. :4112 /gene="Mha1" /number=11 4113. :4257 /gene="Mha1" /number=12 /gene="Mha1" /number=13 /gene="Mha1" /number=1478 /gene="Mha1" /number=1478	/yeue-maa //muber-13 45444636	/gene="Mha1" /number=13 · 4637 . 4875 /gene="Mha1"	/number=14 4876. ,4963 /gene="Mhal"	/number=14 49644996 /gene="Mhal"	/number=15 4997 : 5090 /gene="Mha1"	/number=15 5091 - 5172 /gene="Mhal"	/number=16 5173. 5256 /qene="Mal"	/number=16 52575417 /qene="Mhal"	/number=17 5418. 5512 /qene="Mhal"	/number=17 55135689 /qene="Mha1"	/number=18 56905767 /gene="Mhal"	/numer=18 57685950 /gene="Mha1" /number=19	59516035 /gene="Mal"	//////////////////////////////////////	/evidence=experimental	/evidence=experimental 6409	/evidence=experimental 29 a 2181 c 2086 g 2689 t	8.6%; Score 112.2; DB 8; Length 9285; larity 74.1%; Pred. No. 9.8e-16; Conservative 0; Mismatches 43; Indels 19; Gaps	78 CCGTTCGAGTGACTGCARCATCTTTCTĠCATCGACTTTGTACGGCTACATCGA 137
exon intron exon intron exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	polyA_site	polyA_site	COUNT 2329	Ouery Match Best Local Similarity Matches 177; Conser	78 CCGTTCG 220 CCGTTCG 138 CATATAC
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FVGITTLLIINSTISFIEENNACNAAALWARLAPKAKVLRNGRWAEEESAILVPGDI ISVKLGDIPRADARLLEGDPLKIDQSALTGESLPVTKGPGDGVYSGSTCKQGEIEAVV IATGWHTFFGKAAHLVDSTNOVGHFQKVLTAIGNECISISITYWPTGHRA YRSGIDNLLVLLIGGIPTAMPYLSVTWATIGARRANACHAUFITWMPTGHRA YRSGIDNLLVLLIGGIPTAMPYLSVTWATIGARRANARSTENODAIDATIVGMLDLC SDKTGTLTLNQLTVDKSLVEVFQRGVDQDTVILMAARASRTENODAIDATIVGMLADP TEARAVOEIHPLFPRPPKRRALTLJGGERWHRVSKGABEDGILLLAHNKKDIETRV RAVIDBFARGLRALGVAYQEVPDGRKESPGGPWEFWGILLPLEDPRKDSADTISKAL DLGVNVKMITGDQLAIGKETARRLGMGTNMYPSSALLEDNKDESIDELLETAD GFGAVFPERKYEIVKALQARKHISGWGTNMYPSSALLEDNKDESIDELLETAD GFGAVFPERKYEIVKALQARKHISGWGTVNYTIYAVSITIRIVLGFMLLALIUKFDFPFFM VLITALNDGTIMTISKDRVKFSQPONKNYTIYAVSITIRIVLGFMLLALIUKFDFPFFM VLITALLNDGTIMTISKDRVKFSQPONKNYTIYAVSITIRIVLGFMLLALIUKFDFPPFM FLVAQLIATLIAVANAWAFAAIKGIGWGWAGVIWLINIVLYERGSKSWSVERFGFLLVSA RLVAQLIATLIAVYANWAFAAIKGIGWGWAGVIWLNIVLYEPDIIKKEIRRALGRR AWNLVLEGRIAFTSKNRFGAEERRRWAHAQREHGELQPPERASMERNKTGSSEVN	OLAEERRRAMARSDCCLSSISTERGDQTLHCPV" 15091873 /qene="Mhal"	/number=1 18741993 /gene="Mhal" /number=2	1994 . 2104 /gene="Mhal" /number=2	21052203 /gene="Mhal" /number=3	22042315 /gene="Mhal" /number-3	2316. 2453 /gene="Mha1" /oumber=4	2454 2524 /gene="Mhal"	/number=4 2525. ,2659 /gene="Mhbal" /numbox=8	2560. 2750 /gene="Mha1"	//////////////////////////////////////	7.mm.cr. 2931. /gene="Mhal" /cons_splice=(5'site:no, 3'site:ves)	/number=6 3019. 3225 /gone="Mhal"	//////////////////////////////////////	/number=7 3306. 3425	/gene="Mnal" /number=8 3.25 2500	/sec/sec/sec	35103629 /gene="Mha1" /number=9	36303721 /gene="wha1" /number=9 37223844	/gene="Mhal" /number=10 3845. 3926 /gene="Mhal" /number=10
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RESULT 4 AC108209

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLË

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COMMENT

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Query Match
Best Local Similarity 52.6
Matches 131; Conservative
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Homo sapiens chromosome 4 clone RP11-439B3, WORKING DRAFT SEQUENCE,
7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Jan 31, 2002 this sequence version replaced gi:18376960.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                      -----TC 119
                                                               198 GTAGGGTACATTCTGTTCTTCTTATTGTGCATATTTTTATTGTTGTTTACTGATTATAC 257
                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pleces arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will to be preserved.
                                                                                     Sequencing vector: M13; 2%
Sequencing vector: M13; 2%
Sequencing vector: Diamnid: 98%
Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.990139
Consensus quality: 173471 bases at least Q40
Consensus quality: 173722 bases at least Q30
Consensus quality: 173722 bases at least Q30
Insert size: 173000; agarose-fp
Insert size: 174202; sum-of-contigs
Quality coverage: 12.07 in Q20 bases; sum-of-contigs
Quality coverage: 12.00 in Q20 bases; sum-of-contigs
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1262: gap of unknown length
2346: contig of 1084 bp in length
2446: gap of unknown length
8520: contig of 6074 bp in length
8620: gap of unknown length
24285: contig of 15665 bp in length
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unknown length
of 15665 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- Genome Center ------
                                                                                                                                                                                                                                                                                                                                                   160 CATACACAGAGATGTCTCATGTGAATGGAGCCACTGATG
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
I (bases 1 to 174802)
Waterston,R.H.
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Waterston, R.H.
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PRI 18-JAN-2002
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1 (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll: Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 AAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACT 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%, Score 60.2; DB 2; Length 174802; 52.6%; Pred. No. 0.0033;
24386 63017: contig of 38632 bp in length 63018 63117: gap of unknown length 63018 13781: contig of 50664 bp in length 3782 13781: contig of 50664 bp in length 382 174802: contig of 60921 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF429315 125020 bp DNA linear P
Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   647 others
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig32"
8621. 24285
/note="assembly_name:Contig33"
24386. 63017
/note="assembly_name:Contig34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector_side.right"
113882. 174802
/note="assembly_name:Contig36"
1 33646 c 34740 g 50806 t
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/note="assembly_name:Contig27"
2447. .8520
                                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector_side:left"
63118. .113781
/note="assembly_name:Contig35
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                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                             /clone="RP11-439B3"
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HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWYYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="component of the junctional complex between plasma membrane and endoplasmic reticulum"
                                                                            Tobases 1 to 125020)
Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission
Submisted (05-0GT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16847 GGGACCCAGGTAGTAGCGGCCATCGCARRKMKSHAGRRRMCYYSKSWASWBMSVSYSVK 16906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16907 MHSWHASBSCMHWBKCMTWSCCMSMMYKSSWWGSSWGMCCWGRRRSKGWKWYSRGMSRSK 16966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17207 NTGGGGAAGCTTTTNCNKKTYSYYRKRNGCAMCKYNNYYNNSWRSSCRAGMSCTKYKSSM 17266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         759 ACCCCAACTCTCACCGAAAACCGCGCTGGATCGGCAAATCAAACGAGGTGGTGCCCCGT 818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGTCCGCGCTCGGCAACGAGGCGGCCCGCGCTGAGTCCCCTGGACACCCGACACCC 998
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 A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                 /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
D1sease-Like 2 (HDL2)"
complement(35581..35746)
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4.4%; Score 58; DB 9; Length 125020;
Best Local Similarity 11.8%; Pred. No. 0.01;
Matches 70; Conservative 248; Mismatches 273; Indels 0
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/rpt_unit=ctg
complement(36507. .>36887)
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                                                                                                                                                                                                                                                                                                                                                                                 /product="junctophilin 3"
complement(<36507. .>36887)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="JPH3"
/note="JP3"
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 173848)

Xiong H., Zhou, Y., Dong, H., Lin, W., Chen, B., Zhang, C., Zhang, Y., Cai, Z., Ying, H.F., Wang, H., Gu, W., Zhu, G., Tu, Y., Zhang, X., Jia, J., Shen, H., Zhang, D., Wu, C., Lu, G., Zhong, M., Jiang, H., Ren, S., Fu, G.,
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Bao.J., Bao.W., Blan,X., Cao.T., Chen,C., Chen,J., Ding,H., Dong,W., Fan.H., Feng,X., Gong,J., Guan,O., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,F., Li,F., Li,G., Li,T., Li,Y., Liu,N., Liu,N., Liu,R., Liu,Y., Li,W., Li,
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Submitted (11-FEB-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beljing, Beljing
100101, P.R.China
                                                           TCATGGTCGAGCGTAGCATGCAGGAACTTATTTGCCGTGCGCTCCCAGGTCTCCGCTCGC 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACU9U043 173848 bp DNA linear PRI 11-F
Homo sapiens chromosome 3 clone RP11-551L4 map 3p, complete
sequence.
                                                                                                                                                                                                    1179 GTGCCTTCCAGTCTGTCTCACACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCAGCT
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 501 bases at least 040
Consensus quality: 829 bases at least 040
Consensus quality: 1046 bases at least 020
Insert size: 1157; sum-of-contigs
Quality coverage: 1.35x in 020 bases;sum-of-conti
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/db_xref="taxon:9606"
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http://www.genomics.org.cn
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ACO90043.1 GI:12745081
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Center code: Beijing
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Submitted (04-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jul 1, 2000 this sequence version replaced gi:8653807.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
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Human DNA sequence from clone RP11-382H24 on chromosome 9p22.1-23

Contains a thioredoxin peroxidase pseudogene, a SSB ($51ogren syndrome antigen B (autoantigen La) pseudogene, the 3' end of the MPDZ gene for multiple PDZ domain protein and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169660)
Sehra,H.
                                                                                                                                                                                                                                                                                                                                                                               399 TGTTCTATTTCGAATTTCACTCTATAAACAACATAGTCTACAATGGAAAACAGTGCTTTG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGACTATATACGCGATGTGTGCCTACAACATAAGACAATATAGTCGTTTGAAGATTGA 518
                                                                                                                                                                                     100 TACATCTTTCTGCATCGACTTTGTACGGCTACATCGAACATATACACGAGATGTCTCGTG 159
                                                                                                                                                                                                                                                                     160 TGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCCGTAGGGTACATTCTGTTCTTCT 219
                                                                                                                                                                                                                                                                                                                                                         ATACATATCATCACATATATCACAATATTTTTCTAAATTAAAATTAAAACTAAAAATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 AAATTTCTAACACCAACGACATTGTAATGTTTTCTCCCAACAACTTTACCTAT-TCTACAT
                                                                                                                                             1;
                                                                                                 Length 173848;
                                                                                                                                             Indels
                                                                                                                                           0; Mismatches 234;
                                                                                                     9;
                                                                                                   56.6; DB No. 0.023;
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                 /clone="RP11-551L4"
56663 a 31451 c 31882 g
                                                                                                     Score
Pred.
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HTG; CpG island; MPDZ.
                                                                                                   4.3%;
illarity 47.0%;
Conservative
/map="3p"
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                                                                                                                            Similarity
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                                                                                                                              Best Local Simi
Matches 208;
                                                                                                        Query Match
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AL161449
LOCUS
DEFINITION
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ORGANISM
                                          BASE COUNT
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TITLE
JOURNAL
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KEYWORDS
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http://www.sanger.ac.uk/RGC/Chr9
http://www.sanger.ac.uk/RGC/Chr9
This sequence is the entire insert of clone RPII-382H24 The true
left end of clone RPII-664D14 is at 135950 in this sequence. The
true right end of clone RPII-187K14 is at 53851 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality)
30); an attempt was made to recolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RPII-382H24 is from
the library RPCI-II.2 constructed by the group of Pieter de Jong.
For further details see
on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human echromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="7 copies 60 mer 65% conserved"
2452..2801
/note="175 copies 2 mer ta 61% conserved"
2819..2911
/note="LIMC4 repeat: matches 7864..7961 of consensus"
complement(4102..4478)
/note="match: GSS: Em:AQ180899"
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/note="AluSc repeat: matches 1. .307 of consensus"
7763. .8103
/note="Milial repeat: matches 205. .536 of consensus"
8379. .8422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1589. 1778
/note="MIR repeat: matches 23. .192 of consensus"
1669. 1724
/note="2 copies 28 mer 92% conserved"
2068. 2401
/note="LinkQ repeat: matches 7453. .7834 of consensus 2409. .2828
/note="15 copies 28 mer 62% conserved"
/note="15 copies 28 mer 62% conserved"
/note="2 copies 60 mer 65% conserved"
2452. 2801
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/note="MIR repeat: matches 1. .261 of consensus"
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/note="L1PA12 repeat: matches 5583. .6152 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3379. .8422
/note="22 copies 2 mer tg 86% conserved"
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/note="match: GSS: Em:AQ378047"
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/note=match: GSS: Em:AQ569033"
/note="match: GSS: Em:AQ569033"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-382H24"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/note="L2 re
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| Mote="MLTJJ repeat: matches 33. .189 of consensus" | 18826. .18943 | 1882. . .18943 | 1882. . .18943 | 1882. . .18943 | 1882. . .18943 | 1882. . .18943 | 1882. . .18943 | 18946. . .19291 | 19291 | 19291 | 19291 | 19291 | 19291 | 19292 | 19291 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19292 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 | 19202 |
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/note="match: GSS: Em:B75037"
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28653. .28739
/note="Aludo/FRAM repeat: matches 202. .289 of consensus"
29155. .29237
/note="MIR repeat: matches 97. .194 of consensus"
29262. .29957
/note="L2 repeat: matches 1986. .2742 of consensus"
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/gene="bA382H24.1"
/note="bA382H24.1"
/note="bA382H24.1"
/note="bA382H24.1"
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/note=1s Em:U37125 Em:AF32119
/note=1s Em:U37125 Em:U3
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14831. .15165
/note="match: STS: Em:HS260xAS"
14993. .15072
16682. .16772
/note="MLTD repeat: matches 1. .90 of consensus"
16759. .16999
/note="MLTA] repeat: matches 1. .241 of consensus"
17339. .17648. .18235
/note="Alux repeat: matches 4. .304 of consensus"
17645. .18235
/note="L2 repeat: matches 1961. .2750 of consensus"
18526. .18676
                                                                        consensus
                                                                                                                                                                 .178 of consensus'
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/note="MLT2B repeat: matches 1. .444 of consensus
MLT2B repeat: matches 1. .444 of consensus"
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complement(26637, .27057)
                                                              .309 of
10789. .11105

/note="AluSx repeat: matches 1. .3

/11109 .11267

/note="MERSB repeat: matches 1. .1

complement(12290. .12569)

/note="match: STS: Em:G05562"

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          repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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On Aug 24, 1999 this sequence version replaced gi:5731886.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P. Ealciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL040183.5 GI:5763804
HTG; HTGS_PHASE1.
Malaria parasite P. falciparum.
Plasmodium falciparum falci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ350618
match: STS: Em:G57679"
35089: 35217
/note="L1 repeat: matches 4928. .5057 of consensus"
35239. .36006
/note="L1ME1 repeat: matches 5352. .6103 of consensus"
37784. .37985
/note="L1MC4 repeat: matches 5695. .5897 of consensus"
                        /note="L2 repeat: matches 1771. .1986 of consensus HERVL repeat: matches 5456. .5654 of consensus 30591. .30631. .30631. .30631. .30632. .31387 /note="MLT2A repeat: matches 1. .41 of consensus MLT2A repeat: matches 1. .41 of consensus 30632. .31387 /note="L2 repeat: matches 1156. .1771 of consensus 31401. .31876 /note="MLT1H repeat: matches 13. .516 of consensus 313036. .32142 /note="L2 repeat: matches 929. .1149 of consensus 32790. .33087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424
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50.2%; Pred. No. 0.028;
tive 0; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"AluSx repeat: matches 1.
complement(34142. .34617)
/note-"match: GSS: Em:AQ799891"
34145. .34705
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Best Local Similarity 50.29
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PFMAL13P6
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Homo sapiens clone RP11-115F10, LOW-PASS SEQUENCE SAMPLING.
AC024266
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 65523)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 AAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 TTATACATACATGCACATACATATCATCACATATATCACACAATATTTTTCTAAATT 323
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                                                                                              contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be
                                                                                                                                                                    NOTE: This is a 'working draft' sequence.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                           Order of segments is not known; 800 n's separate segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 204652;
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                                                                                                                                                                                                                                                                                                                                                                                              /strain="3D7"
/db_xref="taxon:5833"
/chromosome="13"
/ 17396 c 17710 g 67856 t 32810 others
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Unpublished
                                                                                                                                                                                                                                                                                                                                            1. .204652
/organism="Plasmodium falciparum"
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0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55.6;
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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HTG; HTGS_PHASE0.
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4.2%;
Best Local Similarity 52.6%;
Matches 121; Conservative (
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                                                                     sequence may
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                                                                                                                                 phage etc.
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AC024266/c
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Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                  Genome
                                                                                                                                                                                                                                                                                                                                                                                         Research
                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                          13302 13301: control of 784 bp in length 13302 14085: contig of 784 bp in length 14086 14185: gap of 100 bp 14186 14181: contig of 796 bp in length 14982 15081: gap of 100 bp 15082 15879: contig of 798 bp in length 15880 15979: gap of 100 bp 15980 16745: contig of 766 bp in length 16746 16845: gap of 100 bp 16846 17645: contig of 800 bp in length 16846 17645: contig of 800 bp in length
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2573 2672: gap of 100 bp
3487 acconting of 100 bp
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808 bp in length
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contig of 744 bp in length
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contig of 791 bp in length
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Web site: http://www-seq.wi.mit.edu
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10720 11503: conti
11504 11603: gap of
11604 12326: conti
12327 12426: gap of
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5298: con
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8832: cor
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6142: co
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7941:
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19448 19547; as one of 100 bp
20177 20476; as control of 703 bp in length
20177 20476; as control of 703 bp in length
20178 21376; control of 703 bp in length
21180 21273; as of 701 of 100 bp
21382 21321; as of 100 bp
21382 21382; as of 100 bp
21382 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCGCGCTGCTGAGTCCCCTGGACACCCGACACCCTGTCGCCCTTTGTTTATTCATCC 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 TAAATCCAAAGTAGGAGCGGTGCATGATGAGAATCGCTCTCAGTACTCGACATAATGAAC 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 CTTACGAGGTACAACAGGCAGGCAGGGACCAGGGGCCGCCTTTATTTCAGGCTCGC 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723 TGGCCCCACGGGCGTGCTGCGTGCACGAAGGGCACTACCCCAACCTCTACCGGAAAACCG 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mitochondrion Schizaphis graminum
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           783 GGCIGGAICGGCAAAICAAACGAGGIGGIGCCCCGIGCCCACITCCCACGICCACGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         843 CATCCCTCTGCAGCCGCTCACCAGCCATGCCGTGTCGCGGAACGGCACAACCACCCCCAA
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36.7%; Pred. No. 0.036;
Live 0; Mismatches 293; Indels 0;
                                                                                                                                   74 54073; gap of 100 bp 100 bp
     in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20860 CGCCCCCCCCCCCCCCGGGGGGGGGGGCCCCCCCC 20818
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f 793 bp
100 bp
f 753 bp
                          8 52327: gap of 100
8 53120: contig of 75
1 53220: gap of 100
53973: contig of 75
4 54073: gap of 100
4 54862: contig of 78
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551202
552228
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553121
553121
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VERSION
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SOURCE
ORGANISM
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SGU36751
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PLN 27-AUG-1999
(ESSA project).
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Beyan, M., Koetter, P., Hempel, S., Entian, K.-D., Bancroft, I., Mewes, H.M., Mayer, K.F.X. and Schueller, C.
            On Mug 24, 1999 this sequence version replaced g1:5731886.
On Mug 24, 1999 this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-MAR-1999) MIPS, at the Max-Planck-Institut fuer
Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
schuelle@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 154818 TAATAATAAAAATATATATATTCTTAATAATAAATTGAACACATTTTAATTTTACATTT 154759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 154638 ATTATATATTTGTATAGATTCTCAATTTAATGCCTATATGAAAAATTGATATT---AA 154582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 CATATATCACAATATTTTCTAAATTAAAATTAAAACTAAAAATGACTAAAATTTCTAACAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 CAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATTGTTCTATTTCGAA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 TAATGCCITAAGCATCGGITACTCCGTAGGGTACATTCTGTTCTTTATTTGTGCATAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITCACTCTATAAACAACATAGTCTACAATGGAAAACAGTGCTTTGTACGACTATATA 470
                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                      phage etc.
Order of segments is not known; 800 n's separate segments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32810 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54.8; DB 2; Length 2
Pred. No. 0.063;
0; Mismatches 142; Indels
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/organism="Plasmodium falciparum"
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EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="13"
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                                                                                                                                                                                                                                                                                                                                                                                                             /strain="3D7"
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Best Local Similarity 51.3%;
Matches 153; Conservative
CB10 1SA, UK
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TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKNKFINIKISENQMIEFIWTTTPPIILIFIAMPTLHLSYSMDEINCPILKIKIFGHO
WFWSYEXSDFSNIEFESYMMNELNKENFRLIVVDNKTIIPFKFNIRLLISSDDVIHSW
TIPSLAIKIDSIPGRMNQINLFMNRPGMYFGQCSEICGINHSFMPIQIESINLNKF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTWLKLSFQNSNSPLMEQLIFFHDHTIFIIMIMTMITYMMIFT
    l (bases I to 650)
Rouhbakhsh, D., Lai, C.Y., von Dohlen, C.D., Clark, M.A., Baumann, L., Baumann, P., Moran, N.A. and Voegtlin, D.J.
The tryptophan biosynthetic pathway of aphid endosymbionts anthranilate synthase (trpEG) within the aphididae
J. Mol. 42 (4), 414-421 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 204652)
Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M.
and Barrell,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 TATATAATA - - ATTTTTACTATAAAAATAAATTTATTAATATTAAAATCTCTGAAAACC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 ACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATTGTTCTATTTTCGAATT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 TATATCACAATTTTTTTTAAATTAAAACTAAAAATGACTAAATTTTCTAACACCA 354
  Aphidiformes; Aphidoidea; Aphididae; Aphidini; Schizaphis.
                                                                                                                                                                                                                                                                                    Idaho State
                                                                                                                                                                                                                                                            Direct Submission
Submitted (20-SEP-1995) Biological Sciences, Idaho Sta
University, Campus Box 8007, Pocatello, ID 83209, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=5
/product="cytochrome oxidase subunit II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
                                                                                                                                                                                                                                                                                                                                                                  /organism="Schizaphis graminum"
/organelle="mitochondrion"
/db_xref="taxon:13262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 TCACTCTATAAACAACATAGTCTACAATGGAAAACAGT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 CTACTCTACATCTTTCATATTCAATAGATGAAATTAAT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAB42168.1"
/db_xref="G1:1036831"
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malaria parasite P. falciparum.
Plasmodium falciparum
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1. 650
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                                                                                                                                                                                                              2 (bases 1 to 650)
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                                                     AUTHORS
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/gene="T25K17.30"
/note="strong similarity to caffeoyl-CoA
O-methyltransferase, Pinus taeda, AF036095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(32558. .32659,32745. .32806,32898. .33006))
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E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosome 4 can be
viewed at: http://websrr.mips.biochem.mpg.de/proj/thai/.
Location/Qualifiers
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PGEDROLMRYTGVKIYPTPYY
PGEDROLMRYTGVKIYPTPYY
PGEDROLMRYTGVKIYPTPYY
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VHIVYSLSKDLGLOFCYRKTHILVSDSDIYSGSYFHASEFTSYAEIVENIDDVSVKRER
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                                                                                                                                                                                                                                 /note="overlap to BAC; please refer to this entry for analysis and annotation"
19417. .19605
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/FC_number="4.4.1.14"

/note="strong similarity to ACC synthase, Malus

domestica, U73816
                                                                                                                              /organism="Arabidopsis thaliana"
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VVFGCIVVSSVLGVVKHRSGLKKISFVAHSLGGLYARYAIGKLYBQPGEVDSLDSPSK
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KHLFLIDMLIISSVDLNSALNAFKRRYAYANRLSMYFDYFYHLOEFALTNEKAMVGM
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                                                                                                                                                       Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemckeemips, biochem.mpg.de_p.mayer@nips.biochem.mpg.de_project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                               Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/Proj/thal/this fragment has an overlap with ATCHRIV63 at the 5' end and an overlap with ATCHRIV65 at the 3' end.

Location/Qualifiers
                            van Staveren, M., Dirkse, W., Stiekema, W., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(6687. .6833,6920. .7036,7083. .7163,7278. .7370,7494. .7733,7782. .7882,7945. .8042,8134.
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/variety="Columbia"
/db_xref="taxon:3702"
                                                                                             4 (bases 1 to 196286)
EU Arabidopsis sequencing, project.
Direct Submission
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/qene="AT4g25770"
                                     Peters, S.A., van Staveren,
Lemcke, K. and Mayer, K.F.X.
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               (bases 1 to 82307)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(33751. .34158,34325. .34648,34729. .34863,34945. .35163)
/gene="T25K17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196286 bp DNA linear PLN 16-MAR-2000 Arabidopsis thallana DNA chromosome 4, contig fragment No. 64. AL161564
                                            /product="putative protein (fragment)"
/product="putative protein (fragment)"
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/number=1
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AKGLRKVKSAYPLVVAILPDVPEEHRQILLAQGCIIREIEPVYPPENKTGYSMAYYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida IBrassicales; Brassicaceae; Arabidopsis.
1 (bases 50686 to 155423; 144355 to 196286)
Rose, M., Hempel, S., Entian, K.-D., Mewes, H.W., Lemcke, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25368 AACATTTATTTTATA--GTAAAATTTTCAATTATATAAAAGTTAAAATTT 25425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25248 ATTAATATTAATAATAATAATTACTAAATAATCATTTATTTGAATTTTGTTTATTATTTT 25307
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Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Mewes,H.W.,
Lemcke,K. and Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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                            'note="contains EST gb:F45349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative protein"
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/db_xref="GI:4539421"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB
Pred. No. 0.08
0; Mismatches
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                                                                                                                                                                                                                                         complement(32745. .32806)
/gene="T25K17.50"
                                                                                                                                                                                                                                                                                                                                                                      .33006)
                                                                                                                                                                                                                                                                                                            .32897)
                                                                                                                                                                                                                                                                                                                                                                        complement(32898.
/qene="T25K17.50"
                                                                                                                                                                                                                                                                                                        complement(32807.
/gene="T25K17.50"
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/gene="T25K17.60"
join(33751. .3415
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/product="putative calmodulin-binding protein"
/product="putative calmodulin-binding protein"
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Bukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 115522)
/gene="AT4g25800"
/note="EST GB:F14385 in 5' untranslated region
strong similarity to calmodulin-binding protein (TCB60)
Nicotianatabacum, PID:g1698548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 169722 AACATITATITATA--GTAAAATTITCAATIATATACAAAGTIAAAAATAAAGTII 169779
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                                                                                                                      contains EST gb:F14386, F14385, N96168, N96141"
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56.6%; Pred. No. 0.097;
.ive 0; Mismatches 90; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=1
14011. .14238
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                                                                                                                                                     /codon_start=1
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14761. .14
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/gne="AT4425780"
/number=1
/gne="AT4425780"
/gne="AT4425790"
/gne="AT4425790"
/mmher=1
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15390. .15595,15645. .16227)
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vakpoplptpspkplilvqppppyvpppgseeqokldphnyvrggilgleplvwdvklas
Yatwwandrrydcsjfhstgpygenlewgsgsdftstfaveswtveaksynhututce
GDGMCGHYTQIVWRETRRLGCARVVCENGAGVFITCNVDPPGNYVGEKPY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="strong similarity to gene PR-1 protein - Medicago truncatula, PIR2:S47171
Contains Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signatures Aal47-157; Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signatures Aal73-184
contains EST gb:226548, Aa586201, Aa712838, Aa712715"
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/gene="AT4@25790"
/omplement/join(10710. .11074,11485. .11752))
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AUTHORS

TITLE JOURNAL

COMMENT

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

TITLE

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.1083,1286. .1597,1804. .2328,2426. .2653)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases ar TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity to other proteins or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Simple repeats were identified by repeatmasker (Arian Smit, Simple repeats were http://ftp.genome.wustl.edu/edy/tRNAscan-SE). Simple repeats were http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                 Lin X., Kaul,S., Rounsley,S.D., Shea,T.P., BenitchM.I., Town,C.D., Reliji,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Ronning,C.M., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.B., Umayam,L., Rallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                          Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA on Dec 17, 1999 this sequence version replaced gi:4335711. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1597,1804. .2328,2426. .>2653)
                                                                                                                                                                                                                                                                        Sequence and analysis of chromosome 2 of the plant Arabidopsis
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Sequence from clone F26H6"

    115522
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                                                                                                                                                                                                                                                                                                                                                 Nature 402 (6763), 761-768 (1999)
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                                                                                                                                                                                                                                                                                                                             thaliana
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source

FEATURES

mRNA gene

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TNSFCVLVNSFYELESAYADFYRSTYAKRANHIGPLSLSNRELGEKARRGKKANIDEO ECLKMLDSKTPGSVVYLSFGSGTNFTNDQLLEIAFGLEGSGQSFIWVYRKNENWGDNB ECLKMLDSKTPGSVYTGSTAFTNDQLLEIAFGLEGSGQSFIWVYRKNENWGDNB PMGARQFYRETTGKGLIFORAPQVLILDHARIGGFVTHCGWNSAIEGIAAGLPMYTW PMGARQFYREKLLFYKTRIGVNVGATELVKKKKLISRAQVEKAVREVIGGEKAEERRR WAKKLGEMAKAAVEEGGSSYNDVNKFWEELNGRK"
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LKLKNIYGTSKNKVAMNLQCSKIFPCKNVELIDINIKQNGVKDGSSTSVCENVDGFAR
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FLKFLESTKYMKQQLESFIETTKPSALVADMFFPWATESAEKLGVPRLVFHGTSFFSL
CCSYNMRIHKPHKKVATSSTPFVIPGLPGDIVITEDQANVAKEETPMGKFMKEVRESE
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Ratural Adams C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabrooks S. L., Amaratunge, H.C., Are, J.R., Banka, T., Barbaria, J., Banton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Amaratunge, H.C., Are, J.R., Banka, F., Burket, C., Blankenburg, K., Bonnin, D., Bouck, J., Burket, C., Burrell, K.L., Byrdin, N.P., Buhay, C., Burch, S., Britea, M., Brown, E., Brown, M., Brown, T., Burket, C., Cherco, T.C., Carron, T.F., Cher, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davis, C., Durbhir, L., Dedarich, D. A., Delaney, K.R., Dedar, G., Chen, R., Day, C., Becotto, M. Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Day, C., Becotto, M., Palls, T., Perraguto, D., Flago, N., Endard, C., Eldar, D., Eddar, D., Eddar, C., Eddar, D., Eddar, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-30AN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 185044 bases at least Q40 Consensus quality: 190296 bases at least Q30 Consensus quality: 194221 bases at least Q30 Estimated insert size: 190368; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 3.5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ç
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Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
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Center clone name: CH230-236F15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .---- Summary Statistics
                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                           AC105576
AC105576.1 GI:18092798
HTG; HTGS_PHASEI; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- Genome Center
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Worley, K.C.
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                                                                                                         Norway rat.
Rattus norvegicus
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                        ACCESSION
VERSION
KEYWORDS
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ORGANISM
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                  AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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14667. .>14757)
/gene="att2g15500"
/gene="att2g15500"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(13713. .13796,13945. .14093,14268. .14303,14375. .14413,
14667. .14757)
/gene="At2g15500"
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VDAQKKERENELKVPYEDSLKETADKFGSYNFRGSGFVAFSTQNVTISGICKDVID
ESVAMPPSYGPRMPIYPLGSPGIRKSPYG"
complement(join(<16628. 18427,18538. 18661,18914. 19100,
19343. 19660,19695. >20682))
                                                                                                                                                                                                                                                                                             /translation="maklearrgakstllttppinakilekpieafkvonpdleigiki
LNFPCVELGLPEGCENRDFINSYQKSDSFDLFLKFLESTKYMKOQLESFIETTKPSAL
VADMEPMATESAEKIGVPRLVFHGTSSFALCCSYNMRIHKPHKKVASSSTPFVIPGL
PGDIVITEDQANVTNEETPFGKFWKEVRESETSSFGVLVNSFYELESSYADFYRSFVA
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EQLLEIAFGLEGSGQNFIWVVSKNENQVGTGENEDWLPKGFEERNKCKGLIIRGWAPQ
VLILDHKAIGGFVTHCGWNSTLEGIAAGLEWYTWPWGAEQFYNEKLLTKYLRIGVNVG
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/protein_id="AAD17394.1"
/db_xref="GI:4335716"
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/protein_id="AAD17393.1"
/db_xref="GI:4335715"
yonn(<11828. .12737,12932. .>13404)
                                                                                                                                          join(11828. .12737,12932. .13404)
/gene="At2g15490"
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Pred. No. 0.096;
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complement(<16628. .>20682)
/gene="At2g15510"
/note="F9013.6"
                                                             <il>1828. .>i3404

                                                                                                                    'note="F9013.4"
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Best Local Similarity 53.38
Matches 136; Conservative
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgso.bcm.tmc.edu/doos/Genbank draft.data.html).
NOTE: This is a "working draft' sequence. It currently consists of 50 contigs. The true order of the pleces is not known and their order in this sequence record is
                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of unknown length
contig of 10459 bp in length
gap of unknown length
contig of 12123 bp in length
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Best Local Similarity 50.8
Matches 128; Conservative
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AASS6S0S ABL34125 ABL34125 AAA70152 AAC16482 AAC1315 AAS61315 AAS61316 AAS656574 ABC34440 AAS49411 AAS49411

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Corn delta-12 desaturase fad2-2 gene 5' untranslated region.
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2. /SIDSI/gcddata/geneseq/geneseqn-embl/NA1981.DAT:*
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1309
1 cccatcgctgctttgtctac.....caagggaaagtgatcccatg 1309
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   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       1736436 segs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                     OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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AAF81468
AAS45444
ABL32458
ABL34124
ABL34224
ABL34241
AAZ17263
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and is derived by analysis of
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Maximum DB &
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Location/Qualiflers 5651..12301 /*tag= a 5439..5444 /*tag= b Е І. (DUPO) DU PONT DE NEMOURS & CO 99WO-US12884 98US-0088987

Masucci JD;

Malven M,

Dubois P,

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Novel promoters isolated from corn for controlling gene expression in male reproductive tissues, such as anthers, tassels, and to regulate transcription of target genes including genes for insect or pathogen
                                                                                                                                                                                                           Claim 1; Page 115-116; 121pp; English.
                                                                      (MONS ) MONSANTO TECHNOLOGY LLC
                       30-APR-2001; 2001WO-US13739.
                                            01-MAY-2000; 2000US-201255P.
                                                                                                                        WPI; 2002-055481/07
08-NOV-2001
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 2
                                                                                                           This is the nucleotide sequence of the 5' untranslated region of the novel corn fad2-2 gene that codes for delta-12 desaturase (see AAX32344). The invention generally relates to the preparation and use of nucleic acid fragments comprising all, or substantially all, of a corn oleosin promoter (see AAX3165-77), a stearoyl-ACP desaturase (see AAX35179-80) and a delta-12 desaturase, which can be used individually or in combination to modify the lipid profile of corn. Suppression of delta-12 desaturase expression can increase the oleic acid content of the seed oil. Also claimed are seeds of such plants, oil obtained from the grain of such plants, animal feed, use of the oil in food, feed, and cooking oil or industrial applications. The promoter region of fad2-2 may be used to express a gene of interest in transgenic corn plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATCGGTTACTCCGTAGGGTACATTCTGTTCTTCTTATTTGTGCATATTTTTATTGTTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITATICA-GACIACCGIICGAGIGACIGCAIGCGIACAICIITCIGCAICGACIIIGI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 ACGGCTACATCGAACATATACACGAGATGTCTCGTGTGAATAGAGTCACTAATGCCTTAA 183
                                                 New maize oleosin promoter, used for producing transgenic plants with altered fatty acid composition of the oil, used e.g. in animal feeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corn; male reproductive tissue; plant regulatory sequence; Zea mays; promoter; transcription regulation; operably linked gene; monocot; dicot; wheat anther; plant fertility; insect tolerance; pathogen tolerance; herbicide tolerance; ds.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                              . 5 TCGCTGCTTTGTCTACATCATGTTCTTCATCATCCTCCCCAGGCGACGCGTGCTGCTGTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 ATATTTTCTAAATTAAAATTAAAACTAAAAATGACTAAATTTCTAACACCAACGA 358
                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                              Score 235; DB 21; Length 12313;
Pred. No. 2.5e-50;
0; Mismatches 60; Indels 2;
                                                                                                                                                                                                                                                                                       Sequence 12313 BP; 2845 A; 2969 C; 3170 G; 3329 T; 0 other;
                                                                                          Example 2; Page 80-84; 108pp; English.
                                                                                                                                                                                                                                                                                                                   18.0%;
82.5%;
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                                                                                                                                                                                                                                                                                                                                            Conservative
                            WPI; 2000-097535/08.
                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                            293;
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         Shen JB;
                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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The present invention relates to the isolation of plant regulatory sequences from the male reproductive tissues of corn (Zea mays). The promoter sequences, fragments, regions or cis elements of the sequences, are capable of regulating transcription of an operably linked DNA sequence. The promoter sequences confer enhanced expression of operably linked genes in monocot or dicot male reproductive tissues, such as arthers, especially wheat anthers and is useful for regulating transcription of a DNA sequence, by operably linking the DNA sequence to the promoter. The promoter sequences are useful in plants to regulate transcription of target genes including genes for control of fertility, insect or pathogen tolerance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation experiments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITATICA-GACIACCGIICGAGIGACIGCAIGCGIACAICIIICIGCAICGACIIIGI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TCGCTGCTTTGTCTACATCTTCTTCATCCTCCCCAGGCGACGCGTGCTGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATCGGTTACTCCGTAGGGTACATTCTGTTCTTATTTGTGCATATTTTATTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ecarcegrecerecereceracaerererrerregrarrrerecar-errrerre
                                                                                                                                                                                                                                                                                                                                                                               plant tissues to identify closely related or homologous genes and associated regulatory sequences. AAS96558-AAS96577 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 232.8; DB 24; Length 2126;
Pred. No. 4.3e-50;
0; Mismatches 57; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGATTATCTGGATTAAAATTAAAACTAAAAATGCCTAACTTTCTAACA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 ATAITITCIAAATTAAATTAAAACTAAAAATGACTAAATTTCTAACA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2126 BP; 607 A; 419 C; 433 G; 667 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              corn promoter sequences of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF81468 standard; DNA; 1888 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.8%;
83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.0
Matches 289; Conservative
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us-09-905-558c-16.rng

(first entry)

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Cell cycle; human; CpG dinuclectide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprocective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle.
                                                                     Chemically pretreated genomic DNA associated with cell cycle #75.
                                                                                                                                                                                                                                                                                                 15-MAR-2001; 2001WO-EP02945
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-602751/68.
                                                                                                                                                                                                                                     WO200168911-A2.
                                                                                                                                                                                                                                                                                                                                                            07-APR-2000; 2
30-JUN-2000; 2
01-SEP-2000; 2
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                               15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                               06-APR-2000;
                                         18-DEC-2001
                                                                                                                                                                                                                                                                    20-SEP-2001
                                                                                                                                                                             PCR primer
              AAS45444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel corn promoter sequences (see AAF81456.AAF81478). The promoter sequences are useful for conferring expression of a second polynucleotide molecule in a transgenic plant tissue. In addition, the promoter sequences are useful for providing selectively modulating expression of any operatively linked gene and provide additional regulatory element diversity in a plant expression vector in gene stacking approaches. The present sequence is one such corn promoter sequence isolated in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                              Novel promoter nucleic acid sequences useful for regulating heterologous gene expression in plants, comprising regulatory sequences located upstream to plant DNA structural coding sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGTTCGAGTGACTGCGTACATCTTTCTGCATCGACTTTGTACGGCTACATCGAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 CATATACACGAGATGTCTCGTGTGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 GTAGGGTACATTCTGTTCTTATTTGTGCATATTTTTATTGTTGTTGTTACTGATTATAC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 TAAATTAAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 ACAACTTTACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACAT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 TCAGCTAATTCTTTGGTGATAGGGTATAAATGACGATGCTCTATATTTATCAGAT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%; Score 124.6; DB 22; Length 1888; larity 63.9%; Pred. No. 4e-22; Conservative 0; Mismatches 114; Indels 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4e-22;
0; Mismatches 114; Indels 14;
                                                                 ds.
                                                       Corn; promoter; transgenic plant; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1888 BP; 569 A; 443 C; 423 G; 453 T; 0 other;
                                                                                                                                                                                                                                                                         Conner TW;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 95; 101pp; English.
                                                                                                                                                                                                                                                                         Ö
                           Corn promoter clone #700342364.
                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                           13-SEP-2000; 2000WO-US25078
                                                                                                                                                                                                          99US-0154182
(first entry)
                                                                                                                                                                                                                                                                    Chay CA,
                                                                                                                                                                                                                                      (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                               WPI; 2001-244796/25
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                                                                                                                WO200119976-A2.
                                                                                                                                                                                                        16-SEP-1999;
                                                                                                                                                                                                                                                                    Anderson HM,
                                                                                                                                               22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227;
                                                                                       Zea mays.
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AAS45444
ID AAS4
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a ð g à g ð a

Berlin K;

2000DE-1013847. 2000DE-1019058. 2000DE-1019173. 2000DE-1032529.

2000DE-1043826

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Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for and/or epigenetic parameters, the differences serving as basis for changed and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, arfaft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2657 TATTGTTGATAGTTTGGATTTTTTAGGTTTTTGTTTTATATATATATATATA 2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 TGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTATACA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50.2; DB 22; Length 6327;
Pred. No. 0.012;
0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6327 BP; 1833 A; 93 C; 1407 G; 2994 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
Claim 1; SEQ ID No 149; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.7%;
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AAS45444 standard; DNA; 6327

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451 GTGCTTTGTACGACTATATACGCGATGTGTGGCTACAACATAAGACAATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1416 TTAATCAAAATACTCTAAACTAACTAACTACAACTAAAAACTACATATATATACA 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAATTICTAACACCAACGACATIGIAAIGTTITCICCAACAACTITACCIAIIC---- 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TACATIGITCTATTICGAATTICACTCTATAAACAACAIGGTCTACAAIGGAAAACA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 ITATITGIGCATATITITATIGITGTTTACIGATIATACGAGTAGITATACATACAIGCA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 CATACATATCATCACATATATCACAATATTTTTCTAAATTAAAATTAAAACTAAAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiantilammatory; cancer; ped Gisease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                             disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, use for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%; Score 50; DB 24; Length 10133; 51.0%; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10133 BP; 3075 A; 70 C; 2051 G; 4937 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 431; 32pp + Sequence Listing; German
                                                                                                                                              Human immune system associated gene SEQ ID NO: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin K;
                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                  ABL32458 standard; DNA; 10133
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-EP07537
                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-2000;
                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2002
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                                                                                     ABL32458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 olek A,
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheinmer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 TCTCCAACAACTTTACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAAATTAAATTAAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 TIATACGAGTAGTTATACATACATGCACATACATATCATCACATATATCACAATATTTT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                           immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
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Sequence 73334 BP; 18968 A; 858 C; 15329 G; 38179 T; 0 other;
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                                                                                                                                                                   BP.
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                                                                                                                                                                      ABL34124 standard; DNA; 73334
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                (first entry)
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Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200200928-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; ds.
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(CHIR ) CHIRON CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crkvenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9938972-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1998;
03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1998
24-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ17263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-)
                                                                 6819
                                                                                                                                                                                         6229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
including eye diseases such as retinopathy, neovacular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epllepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6878 TAATICTAAATACTACATATACATTTTAAATATAACTC-ATTAAATATACACAAAAAAT 6820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 TATTIGIGCATATITITATIGITGITTACTGATTATACGAGTAGTATATACATACATGCAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCCGTAGGGTACATTCTGTTCTTCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 ATACATATCATCACATATATCACAATATTTTTTTAAATTAAATTAAACTAAAAAGACT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic; antiarterlosclerotic; antianaemic; cytostatic; noctropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antifheumatic; antiarthitic; antidiabetic; antiarthitic; antidiabetic; antisposiatic; antilnflammatory; cancer; eye disease; arterlosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2214; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11691 BP; 3695 A; 49 C; 1861 G; 6086 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 2214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 133;
                                                                                                                                                                                                      RESULT 7

ABL34241/c

ID ABL34241

XX

AC ABL34241;

XX

C ABL34241;

XX

DE Human immune system associated gene XX

Human; immune system disease; cytosi antiarteriosclerotic; antianaemic; contranaemic; contranae
                                                                                              | |||| || ||
59055 TCATCTATCATATAA 59041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%;
51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 140; Conservative
                                                                 432 TAGTCTACAATGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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The present invention describes a library of human polynucleotides comprising the sequences given in AA212532 to AA21779. Also described is comprising the sequences given in AA212532 to AA21779. Also described is a method of detecting differentially expressed genes correlated with the differentially expressed gene product in a test sample from a cell cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotides sequences given in AA212532 to AA217779. The polynucleotides can be used for a variety of purpose, e.g. detection of expression levels, can be used for raising or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and thermaly also be used to construct carrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as
340 AAATTICTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                   Human gene expression product cDNA sequence SEQ ID NO:4735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R, Dickson M, Drmanac R, Drmanac S;
Garcia PD, Garcia V, Giese K, Innis MA;
assam A, Kennedy GC, Kita D, Labat I;
eshkowitz D, Pot D, Randazzo F, Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leshkowitz D, Pot D, Randazzo F, Re
n B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                        6699 TITCAAAATAATTIACACAATAAAAAAAATACA 6666
                                                                                                                                400 GITCIATTICGAATTICACTCIATAAACAACATA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2250-2251; 2479pp; English.
                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                AAZ17263 standard; cDNA; 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US01619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0080515
                                                                                                                                                                                                                                                                                                                                           12-OCT-1999 (first entry)
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Jones WL, Kassam A,
Loshkowitz
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DB 22; Length 399; 0.013;

Pred. No. 0.013; 0; Mismatches 165;

Score 48;

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448 ACAGTGCTTTGTACGACTATATACGCGATGTGTGGCTACAACATAAGACAATATAGTCGT 507
                                                                                                                                                                                       208 TICTGTICTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTAT 267
                                                                                                  268 ACATACATGCACATACATCATCACATATATCACAATATTTTTCTAAATTAAATTAAAA 327
                                                                                                                                                                                                                                                                                     328 CTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCCAACAACTTAAC
                                                                                                                                                                                                                     388 CTATICTACATIGITCTATITCGAATITCACTCTATAAACAACATAGICTACAAIGGAAA
                                                                                                                                                                                                                                         Sequence 399 BP; 225 A; 24 C; 15 G; 135 T; 0 other;
                                                      47.18;
                                                       Best Local Similarity 47.1
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                TIGAAGAIIGAA 519
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(AAH93283-AAH93356).
                                                                                                                                                                                                                                                                                                                               || || || TTAAATTATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200170976-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAS56505;
                                              Query Match
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                                                                                                                                                                                                                                                                                                                  508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated human polynucleotide (AAH75398) encoding a novel polypeptide (AAG64527) useful in antiense-therapy and gene-therapy, in diagnostics, forensics, gene mapping and identification of mutations responsible for genetic disorders and other traits. Polynucleotide sequences with potential homology were also identified
    cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                              965 CCGCGCTGCTGAGTCCCCTGGACACCCGACACCCTGTCGCCCTTTGTTTATTCATCCG 1024
                                                                                                                                                                                                                                                                                   905 CACTCACGAAACCCCGTCCCGGCCGTGTCGGTCCGCTCGCCTCGGCAACGAGGCGGC 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                             785 CIGGATCGGCAAATCAAACGAGGTGGTGCCCCGTGCCCACTCTCCACGTCCACGGCACCA 844
                                                                                                                                                                         845 ICCCICIGCAGCCGCICACCAGCCATGCCGTGTCGCGGAACGGCACAACCACCCCCAACC
                                                                                                         ô
                                                                                    Length 1337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antisense-therapy; gene-therapy; diagnostic; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum MAL3P8 polynucleotide SEQ ID NO 16.
                                                                                                          Indels
                                                             Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
                                                                                                                                                                                                                                                                                                           1025 AAATCTCATCTGCCCCCACGGCCGACTGCGCTGCGCCGCCC 1065
                                                                                                                                                                                                                                                                                                                         , 621 CCCNCCNCCCCCCCCCCNNNNCCCCCCCCCCCCCCC 661
                                                                                     3.7%; Score 48.4; DB 20;
34.5%; Pred. No. 0.018;
iive 0; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 106; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-2000; 2000WO-US35190
                                                                                                                                                                                                                                                                                                                                                                                           AAH93294 standard; DNA; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                   Local Similairy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-451890/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene mapping; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200152616-A2
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                                                                                          Query Match
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                                                                                                                Matches
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The invention relates to human polynucleotides encoding proteins associated with ovarian and endometrial cancers. The polynucleotides and the proteins they encode may be used in the prevention, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 222 polypeptides associated with ovarian and endometrial cancers, useful for diagnosing, preventing and treating
                                                                                                                                                                                                                                          Human: ss; ovarian cancer protein; cancer; tumour; ovarian cancer; endometrial cancer; cytostatic.
                                                                                                                                                                                         Human cDNA for an ovarian cancer protein #129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 157; 187pp; English.
                BP.
505/c
AAS56505 standard; cDNA; 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000; 2000US-190710P.
22-JUN-2000; 2000US-213748P.
19-DEC-2000; 2000US-257276P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2001; 2001WO-US09062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyle RA, Stolk JA;
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
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treatment of diseases associated with the inappropriate expression of ovarian and endometrial cancer polypeptides (OECPS). For example, the polynucleotide (or am expression vector comprising the polynucleotide) and the OECP may be used to treat disorders associated with decreased that affect the activity of OECPs by expressing inactive proteins or to upplement the patients own production of them. Additionally, the supplement the patients own production of them. Additionally, the polynucleotide may be used to produce the OECPs, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotide and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in the production of anti-OECP antibodies and in assays to identify and anti-OECP antibodies and in assays to identify antiandiators of it's expression and activity. The anti-OECP antibodies and requisite expression and activity. The anti-OECP antibodies and a midgonists may also be used to down regulate expression and activity. The anti-OECP antibodies may also be used as diagnostic agents for immunosorbant assay (ELISA)) and hence diagnose patients with cancers. The present sequence is a ovarian and endometrial cancer linked cancers. The present sequence is a ovarian and endometrial cancer linked.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 TGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTATACA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 TITITITITITITITITITITITICAGGGATTGAACACATTITITAATTATTAGAAATACA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 AAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 2098.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 326 BP; 130 A; 48 C; 34 G; 114 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
0.014;
77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL34125 standard; DNA; 73334 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000; 2000DE-1032529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.0
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disporders, including eye diseases such as retinopathy, necvascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                      411
                                                                                                                                                                                                                                                                                                                                                                                        232 TITITATIGITGTTTACIGATTATACGAGTAGTTATACATACATGCACATACATATCATC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 ACATATATCACAATATTTTTCTAAATTAAAATTAAAACTAAAAATGACTAAAATTCTAACA 351
                                                                ising fragment of chemically modified gene, useful treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer: eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psorlasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 CCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATTGTTCTATTTCGA
                                                                                                                                                                                                                                                                                                                                    Length 73334;
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                              Sequence 73334 BP; 24605 A; 858 C; 14432 G; 33439 T; 0 other;
                                                                                                                       Claim 1; SEQ ID NO 2098; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune system associated gene SEQ ID NO: 1547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66098 AAATCACTTAATCCCAAAAATTCGAATCCAACGTAAACA 66060
                                                                                                                                                                                                                                                                                                                                  DB 24;
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 ATTTCACTCTATAAACAACATAGTCTACAATGGAAAACA 450
                                                                                                                                                                                                                                                                                                                                  Score 47.8; DB Pred. No. 0.15;
   Berlin K;
                                                                                                                                                                                                                                                                                                                             3.7%;
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2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 51.1
Matches 112; Conservative
   ပဲ
                                                                comprising
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 Piepenbrock
                                                                                            cytosine methylation
                             WPI; 2002-130909/17.
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                                                             Nucleic acid
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01-SEP-2000;
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Olek A,
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                                                                                                                   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reunamia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                6271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487
                                                                                                                                                                                                                                                                                                             6510 TACTCTTTAAAATACCTACTAATTCTCAATTCCTTTCATCCTAACATTAACCCTAAATAA 6451
                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:285
                                                                                                                                                                                                                                                                                                                                    252 TIATACGAGTAGTTATACATACATGCACATACATATCATCACATATATCACAATATTTT 311
                                                                                                                                                                                                                                                                                                                                                                                 367
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                                                      comprising fragment of chemically modified gene, useful and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                               6330 ATAATCTAAAAAACCTAAAACTCCATAATCATTACTAAACATAAACTATCAATTAATCCTT
                                                                                                                                                                                                                                                                                                                                                                                 CTAAATT - - - - AAATTAAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                            GTTTTCTCCCAACAACTTTACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAAC
                                                                                                                                                                                                                                                                                                                                                                                                      428 AACATAGTCTACAATGGAAAACAGTGCTTTGTACGACTATATACGCGATGTGGCTACA
                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                              DB 24; Length 6627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      falciparum; chromosome 2; human malaria parasite;
11; malaria; protozoacide; infection; insecticide;
                                                                                                                                                                                                                         Sequence 6627 BP; 2052 A; 117 C; 1386 G; 3072 T; 0 other;
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0.066;
~hes 156; Indels
                                                                                                   Claim 1; SEQ ID NO 1547; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                Score 47.4;
                                                                                                                                                                                                                                                             Pred. No.
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                                                                                                                                                                                                                                                 3.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6210 CCAATCGAAAACTA 6196
                                                                                                                                                                                                                                                                      Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 ACATAAGACAATATA 502
                                                         Nucleic acid comprising
              Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimalarial; malaria;
                                                                               cytosine methylation
                                   WPI; 2002-130909/17
                                                                                                                                                                                                                                                           Local Similarity
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                                                                      diagnosis
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                                                                                                                                                                                                                                                  Query Match
               olek A,
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The present invention describes proteins and their inaquences (I) elected by chromosome 2 of the human malarial parasite, plasmodium falciparum. Also described are: (I) nuclectide sequences (II) encoding (I): and (2).

Also described are: (I) nuclectide sequences (II) encoding (I): and (2).

Covaccines against P. falciparum infection comprising (I) or (II).

Covaccines against P. falciparum infection (II) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially when they are rifins or secreted or membrane proteins) (I) (especially development of fargs to precess hampered by the complexity of the parasitic lifecycle, and provide new targets for resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new parts of the world, and there is a pressing need for vaccines and new and protein sequences given in the present invention, but which are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2403 TTTTGAAAATTCATTCAATATATATTTCATATAATTGAAAGATATTATACACATTCCA 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2523 ACARICITITICIANGTACAACCATATITATATAATATTATTATATATATATAGTTATACT 2464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 TATACATACATGCACATACATATCATCATATATCACAATATTTTTCTAAATTA
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                                                                                                                                                                                                                                                                                                                        Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes proteins and their fragments (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47.2; DB 21; Length 6033;
Pred. No. 0.071;
0; Mismatches 123; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection
                                                                                                                                                                             Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 493-495; 577pp; English
                                                                                                                                                                                 Gardner M,
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                                                                                                                                                                                     'n
                                                                                                                                                                                     Carucci
                                                                                                                                                                                                                                                          WPI; 2000-365347/31
HOFFMAN S.
CARUCCI D.
GARDNER M.
                                                                                                           VENTER J C.
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                                                                                                                                                                                     Hoffman S,
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       (HOFF/)
                                                                                                               (VENT/)
                                                                             (GARD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                   The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancers by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for potentially preventing monitoring, characterising treating and polypeptides are also useful for isolating compounds with cytostatic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 GTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTATACAT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATGCACATACATATCATCACATATATCACAATATTTTTCTAAATTAAAATTAAAACTAA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                          New peptide useful as a marker for the diagnosis of breast cancer
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Pred. No. 0.023;
0; Mismatches 77; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 TATGGCTTAAAATTGAAATTTCATAGACATGTAATTTTATTCCCTAAAAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 AAAIGACTAAATITCTAACACCAACGACATIGTAAIGTITICTCCAACAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene regulation-associated gene oligonucleotide #270.
Human breast cancer expressed polynucleotide 8939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 281 BP; 93 A; 32 C; 39 G; 117 T; 0 other;
                      breast cancer; cell marker; cytostatic;
                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                 Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                Claim 1; Page 1617; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                               2000US-0189167.
2000US-0192099.
2000US-0193480.
2000US-0205230.
2000US-0211315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.68;
54.78;
                                                                                                                                                                                                     2000US-0220534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS61315 standard; DNA; 6107
                                                                                                             10-JAN-2001; 2001WO-US00798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93; Conservative
                                                                                                                                                                                                                                                                      WPI; 2001-451856/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                               Xu Y,
                                                                  WO200151628-A2
                                                                                                                                                                             15-MAY-2000;
09-JUN-2000;
25-JUL-2000;
                                              Homo sapiens
                                                                                                                                                                    29-MAR-2000;
                                                                                                                                    14-JAN-2000;
                                                                                                                                               L4-MAR-2000;
                                                                                                                                                          24 - MAR - 2000;
                                                                                       19-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2002
                                                                                                                                                                                                                                              Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                      Human;
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The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene requiation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the chemical pretreatment converts cytosine bases unmethylated at the classifier to cytosine, to enable analysis of cytosine methylations. Cf dissimilar to cytosine, to enable analysis of cytosine methylations. Cf dissimilar to cytosine, to enable analysis of cytosine methylations. Cf useful in the diagnosis of diseases (or predisposition to diseases) associated with gene requiation and in therapy of such diseases, cardiac associated with gene combined immunodeficiency disease, cardiac chick are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, cathma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, precalampsia, graft versus-host disease. The present sequence is a sequence data for this specification and is solid the printed specification, but was obtained in electronic of the printed specification, but was obtained in electronic fip. wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2615 ITTATATATATATATATATATATATATATATACATTITTATTACACACAAACTCTATC 2556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1033529.
01-SEP-2000; 2000DE-1043826.
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nes 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                        WO200177375-A2.
                                                                                                                                                         Homo sapiens
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Search completed: November 7, 2002, 10:50:17 Job time : 319.436 secs

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Sequence 14, Appli
Sequence 14, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 63, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 96, Appli
Sequence 96, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 5, Appli
Sequence 21, Appli
Sequence 22, Appli
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Sequence 24, Appli
                                                                  7, 2002, 07:44:03; Search time 38.9851 Seconds (without alignments) 8247.617 Million cell updates/sec
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                                                                                                                                              1 cccatcgctgctttgtctac.....caagggaaagtgatcccatg 1309
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'Ggn2_6/ptodata/1/ina/5A_COMB.seq:*
'Cgn2_6/ptodata/1/ina/5B_COMB.seq:*
'Cgn2_6/ptodata/1/ina/6A_COMB.seq:*
'Cgn2_6/ptodata/1/ina/6B_COMB.seq:*
'Cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
'Cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
'Cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-08-74-522-4
US-09-007-119-10
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US-08-007-119-10
5312912-3
US-08-91-94-63
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US-08-91-94-63
US-08-91-92-96
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US-08-91-927-5
US-09-165-24-11
US-09-165-24-13
US-09-165-22
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                                                                                                                                                                                                            383533 seqs, 122816752 residues
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                                             - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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c 28 38.4 2.9 1736 4 US-09-634-530-24 3 9 38.4 2.9 4253 3 US-09-634-530-24 3 1 38.2 2.9 4253 3 US-09-634-483-7 3 1 38.2 2.9 4256 3 US-09-634-483-7 3 3 8.2 2.9 4256 3 US-09-634-18-4 3 3 8.2 2.9 4256 3 US-09-881-094-4 3 4 37.8 2.9 999 1 US-09-389-982-98 3 5 7.8 2.9 999 1 US-09-389-982-98 3 7 7.8 2.9 999 1 US-09-389-982-98 3 7 7.8 2.9 999 3 US-09-389-982-98 4 1 27.8 2.9 999 3 US-08-040-13-4 4 3 7.8 2.9 999 3 US-08-040-13-4 4 3 7.8 2.9 999 3 US-08-034-3 4 3 7.8 2.9 999 3 US-08-034-3 4 3 7.8 2.9 999 3 US-08-034-3 4 4 3 7.8 2.9 999 3 US-08-034-3 4 4 3 7.8 2.9 999 3 US-08-034-3 4 4 3 7.8 2.9 999 4 US-08-034-3 4 4 3 7.8 2.9 999 4 US-08-034-3 4 5 7.8 2.9 999 3 US-08-034-3 4 5 7.8 2.9 999 4 US-08-034-3 4 7 7.8 2.9 999 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 2 2 9 925 7 US-08-034-3 4 8 7 18 18 18 18 18 18 18 18 18 18 18 18 18	Sequence 22, Appl Sequence 24, Appl Sequence 7, Appli Sequence 4, Appli Sequence 4, Appli Sequence 9, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli		
0	28 38.4 2.9 1736 4 31 38.4 2.9 1736 4 31 38.2 2.9 4523 3 32 38.2 2.9 4526 2 34 38.2 2.9 4526 2 34 37.8 2.9 899 1 37 37.8 2.9 899 1 37 37.8 2.9 899 3 37 37.8 2.9 899 3 37 37.8 2.9 899 4 41 37.8 2.9 899 3 40 37.8 2.9 899 3 41 37.8 2.9 899 4 41 37.8 2.9 899 4 41 37.8 2.9 899 4 41 37.8 2.9 899 4 42 37.8 2.9 899 4 41 37.8 2.9 899 4 43 37.8 2.9 899 4 43 37.8 2.9 899 5 44 37.8 2.9 899 5	14, Application US/08232463 15, Application US/08232463 INFORMATION: ANT: DORNER, F. ANT: SCHEIFLINGER, F. ANT: SCHEIFLINGER, F. ANT: SCHEIFLINGER, F. ANT: SCHEIFLINGER, F. ANT: SCHOOLES: 52 CONDENCE: 52 CONDENCE: ADDRESS: SSEE: FOLEY & Lardner TT: 1800 Diagonal Road, Suite 500 3: VA RY: USA 12313-029 RR READABLE FORM: MITTE: FOLEY & disk	### Section #1.2

DB 1; Length 7218;

3.9%; Score 51.2;

Query Match

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OTHER
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                                                                                                                                                                                                                                                    791 CGGCAAATCAAACGAGGTGGTGCCCCGTGCCCACTCTCCACGGCACGATCCCTC 850
                                                                                                       851 TECAGCCECTCACCAGCCATGCCGTGTCGCGGAACGGCACAACCACCCCCAACCCACTCA 910
                                                                                                                                                                    CGAAACCCCGTCCCGGCCGTGCCCGTCGGCTCGGCAACGAGGCGGCCCGCGC
              0;
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                Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08749522
Patent No. 6096950
GENERAL INFORMATION:
APPLICANT: John, Mallyakal
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
STREET: Quarles & Brady
STREET: 411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                       1151 TGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCA 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Baker, Jean C.
REGISTRATION NUMBER: 57,433
RECENENCE/DOCKET NUMBER: 670513.90244
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
ilarity 4.3%; Pre
Conservative 219;
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STRANDEDNESS: double
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CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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 Best Local Similarity
Matches 17; Conserv
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US-08-749-522-4/c
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DB 3;

3.3%; Score 43.4;

Query Match

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Sequence 14, Application US/09007119C

Sequence 14, Application US/09007119C

Patent No. 6300541

GENERAL INFORMATION:

APPLICANT: Lighthoot, David A.

APPLICANT: Merkem, Khalid

TITLE OF INVENTION: Soybean Sudden Death Syndrome Resistant Soybeans,

TITLE OF INVENTION: Soybean Cyst Nematode Resistant Soybeans and Methods of

TITLE OF INVENTION: Soybean (Soy Nomatode Resistant Plants)

TITLE OF INVENTION: Soybean (Soy Nomatode Resistant Plants)

FILE REFERENCE: Sou Illinois 1268/2 Sequence Listing

FAILER PREPAICATION NUMBER: US/09/007,119C

CURRENT FILING DATE: 1998-01-14

EARLIER APPLICATION NUMBER: 60/035,335

EARLIER PRILING DATE: 1997-01-14

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                           288 CATCACATATATCACAATATTTTTCTAAATTAAAATTAAAACTAAAAATGACTAAAATTTCT 347
                                               348 AACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATTGTTCTATT
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pred. No. 0.018;
); Mismatches 101;
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OTHER INFORMATION: (a or c or g or t/u)
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Best Local Similarity 50.7%;
Matches 104; Conservative
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OTHER INFORMATION: (a or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (677)...(678)
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE.
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-007-119-14
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281 TACATATCATCACATATATCACAATATTTTTCTAAATTAAAATTAAAACTAAAAATGACTA 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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Pred. No. 0.041;
0; Mismatches 77; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES FOR GENETICALLY ENGINEERING DISEASE RESISTANCE AND OTHER INDUCIBLE TRAILY ENGINEERING DISEASE RESISTANCE AND OTHER NUMBER OF SEQUENCES: 9 CURRENT APPLICATION DATA: 18701/393,301 FILING DATE: 13-UN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
3.3%; Score 43; DB 4; Length 809;
Best Local Similarity 54.8%; Pred. No. 0.012;
Matches 85; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5312912-3/c;Patent No. 5312912; APPLICANT: HADWIGER, LEE A.;CHIANG, CHIN C.;HOROVITZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 AATTTCTAACACCAACGACATTGTAATGTTTCTC 375
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LOCATION: (747)
OTHER INFORMATION: (a or c or g or t/u)
                                                                                                                LOCATION: (662)
OTHER INFORMATION: (a or c or g or t/u)
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                             g or t/u)
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OTHER INFORMATION: (a or c or g or t/u)
FEATURE:
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; OTHER INFORMATION: (a or c or g or t/u)
US-09-007-119-10
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                                                        OTHER INFORMATION: (a or c or g
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OTHER INFORMATION: (a or c or PEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (785)
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Best Local Similarity 53.3%;
Matches 88; Conservative
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                   misc_feature
(619)
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: (769)
                                                                                                 NAME/KEY: misc_feature
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LOCATION: (797)
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Sequence 10, Application US/09007119C

Patent No. 6300541

GENERAL INFORMATION:
APPLICANT: Lighfoot, David A.
APPLICANT: Gibson, Paul T.
APPLICANT: Gibson, Paul T.
APPLICANT: Gibson, Paul T.
APPLICANT: McKem, Khalid
TITLE OF INVENTION: Soybean Cyst Nematode Resistant Soybeans,
TITLE OF INVENTION: Soybean Cyst Nematode Resistant Soybeans and Methods of
TITLE OF INVENTION: Breeding and Identifying Resistant Plants
FILE REFERENCE: Sou Illinois 1268/2 Sequence Listing
FILE APPLICATION NUMBER: US/09/007,119C

CURRENT APPLICATION NUMBER: GO/035,335

EARLIER FILING DATE: 1997-01-14

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 4; Length 796;
Pred. No. 0.012;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 TATTTCTAAAATGTCCTTCATTGGAACTTGTTATC 302
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                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (771)..(772)
OTHER INFORMATION: (a or c or g or t/u)
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                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (792)
OTHER INFORMATION: (a or c or g or t/u)
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; OTHER INFORMATION: (a or c or g or t/u)
US-09-007-119-14
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LOCATION: (710)
OTHER INFORMATION: (a or c or g or FEATURE:
NAME/KES: misc_feature
LOCATION: (723)
OTHER INFORMATION: (a or c or g or
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Best Local Similarity 54.8%;
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LOCATION: (1)...(6)
OTHER INFORMATION: (a or
FEATURE:
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LOCATION: (787)
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LOCATION: (796)
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US-09-007-119-10/c
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Gaps

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PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: FETDER, DONIA M. 826ISTRATION NUMBER: 33878
REFERENCE/DOCKET NUMBER: 69-9.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4254 base pairs
                                                                                     E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                          18-MAY-1995
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Best Local Similarity 52.77
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                      COMPUTER READABLE FORM:
                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Boulder
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MOLECULE TYPE:
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                                                                                                                                                                                                  FILING DATE:
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COCATION:

US-08-443-639-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 TGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTATACA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTA 390
                   292 ACATATATCACAATATTTTTTTTAAATTAAAATTAAAACTAAAAATGACTAAAATTTCTAACA 351
                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                               352 CCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTAC 396
                                                                                                                                                                                                  168 CTGTCATAATTATTTTCTTTTTTAACTACTTAACCCTTATGAC 124
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Pred. No. 0.04;
0; Mismatches 119;
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STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
TILE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                     Sequence 63, Application US/08821994A Patent No. 6228643 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08443639
Patent No. 5981843
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 3.2%;
Best Local Similarity 48.7%;
Matches 113; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA; OAGANISM: Brassica napus
US-08-821-994-63
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US-08-443-639-7/C
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Sequence 1, Application US/08973462B

Sequence 1, Application US/08973462B

Patent No. 6191270

GENERAL INFORMATION:

APPLICANT: DRILHE, PIERRE

APPLICANT: DAUBERSIES, PIERRE

TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

FILE REFERENCE: 066-0125-0 PCT

CURRENT APPLICATION NUMBER: US/08/973,462B

CURRENT PILING DATE: 1998-02-06

EARLIER APPLICATION NUMBER: PCT/FR96/00894

EARLIER APPLICATION NUMBER: FR 95/07007

EARLIER PILING DATE: 1995-06-13

NUMBER: OF SEQ ID NOS: 29

SEQ ID NO 1

SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 AAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCCAACAACTT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 TATACATACATGCACATACATATCATCACATATATCACAATATTTTTCTAAATTAAATTA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 TACCTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACATA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..2477, 2609..2747, 2903..3148, 3262..3558)
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2259
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,639
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237 IGTCACTCTATTATTTAATATCATAAAATACATGAAAATACATTTTCTGTAGAATCAC 296
                                                                                                                                                                                                                                                           297 GITITCCTCCTACTGTGAATAAAGACATAACTCACTAAGGGGAAGAATCTTGGCCCNAAG 356
                                                                     268 ACATACATGCACATACATATCATCACATATATCACAATATTTTTTTAAATTAAAA 327
                                                                                                                                             328 CTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTAC
                                                                                                                                                                                                                       388 CTATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACATGGTCTACAATGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%; Score 40.4; DB 5; Length 1 46.4%; Pred. No. 0.072; tive 0; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHOD TO DIAGNOSE HEREDITARY HEMOCHROMATOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA; PAPLICATION NUMBER: PCT/US96/06352 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/599,252 FILING DATE: 09-FEB-1996 ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9053-0001.21
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 96, Application PC/TUS9606352
GENERAL INFORMATION:
APPLICANT: DRAYNA, DENNIS T.
                                                                                                                                                                                                                                                                                                 448 ACAGTGCTTTGTACGACTATATA 470
                                                                                                                                                                                                                                                                                                                                     357 TGTGTGATAAATCANANAANANA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FEDER, JOHN N.
APPLICANT: RIMBEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: THOMAS, WINSTON J.
TITLE OF INVENTION: METHOD TO D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 905
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 2006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 46.48
Matches 122; Conservative
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EDNESS: single
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ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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PCT-US96-06352-96
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                                                                                                                                                                                                     199 TAGGGTACATTCTGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACG 258
                                                                                                                                                                                                                                           208 ITCTGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTAT 267
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                                                                                                     Length 6152;
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Similarity 46.4%; Pred. No. 0.072;
22; Conservative 0; Mismatches 141; Indels (
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FEDER, JOHN N.
APPLICANT: GNIKKE, ANDREAS
APPLICANT: THOMAL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
CORRESPONDENCE ADDRESS: 124
                                                                                             Score 40.6; DB 4;
Pred. No. 0.16;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/599,252 FILING DATE: 09-FEB-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                             5889 TTCTTACAGAAATCTATATATAAAAA 5859
                                                                                                                                                                                                                                                                                                                   319 AAATTAAAACTAAAAATGACTAAATTTCTAA 349
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ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 96, Application US/08599252
Patent No. 5705343
GENERAL INFORMATION:
APPLICANT: DRAYNA, DENNIS T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
METEREX: (202) 887-1500
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 96: SEQUENCE CHARACTERISTICS: LENGTH: 1000 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                         Query Match
Best Local Similarity 54.3%;
Matches 82; Conservative
             TYPE: DNA
ORGANISM: P. falciparum
US-08-973-462-1
LENGTH: 6152
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Best Local Simi
Matches 122;
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                                                                                  328 CIAAAAAIGACIAAAITICIAACACCAACGACAIIGIAAIGITITCICCAACAACITIAC 387
                                                                                                                                                  237 TGTCACTCTATTATATTATATATAAAAATACATGAAAATACATTTTTCTGTAGAATCC 296
                                                                                                                                                                                              388 CIATICTACATIGITCTATITCGAATTICACTCIATAAACAACAIAGICTACAAIGGAAA 447
           117 TTATTTATTATTAAAAATAATATTTAATATTAAATATTAATTTATTATTATTATTAT 176
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STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FEDER, JOHN N.
APPLICANT: GNIRKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
APPLICANT: METHON TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06583
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ER: 9053-0001.21
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APPLICATION NUMBER: US 08/599,252
FILING DATE: 09-FEBS-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 96, Application PC/TUS9606583
GENERAL INFORMATION:
APPLICANT: DRAYNA, DENNIS T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            448 ACAGTGCTTTGTACGACTATATA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RATIONALIS HOUSERS 19,959
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 9053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                357 TGTGTGATAAATCANANAANANA 379
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IBM PC compatible
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INFORMATION FOR SEQ ID NO: 9
SEDGENCE CHARACTERISTICS:
LENGTH: 1000 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.1
Best Local Similarity 46.4
Matches 122; Conservative
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CORRESPONDENCE ADDRESS:
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208 TTCTGTTCTTCTTATTGTGCATATTTTTATTGTTTACTGATTATACGAGTAGTTAT 267

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388 CTATICTACATIGITCTATITCGAATITCACTCTATAAACAACATGGTCTACAAIGGAAA 447
                                                                                                                                                                                                                          328 CTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTAC 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: One Commerce Square, 2005 Market Street, 22nd
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08972927
Patent No. 6166290
GENERAL INFORMATION:
APPLICANT: Rea, Philip A
APPLICANT: Lu, Yu-Ping
APPLICANT: Li, Ze-Sheng
TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT:
ITILE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/031,040
FILING DATE: 18-NOV-1996
PRIOR APPLICATION NUMBER: US 60/061,328
FILING DATE: 08-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEATY Ph.D., Kathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/972,927
18-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 1910-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                     448 ACAGTGCTTTGTACGACTATATA 470
                                                                                                                                                                                                                                                                                                                          357 TGTGTGATAAATCANANAANANA 379
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TELEPHONE: 215-965-1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Philadelphia
STATE: Pennsylvania
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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US-08-972-927-5/c
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3487 ITCATATITITITAACGAITITITITITAACTATITITITAACTAATIGICICGITA 3546
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                                                                                                                                                                                                                                                                                                      264 TIATACATACATGCACATACATATCATCACATATATCACAATATTTTTCTAAATTAAATT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hoffman, Stephen L.
APPLICANT: Charoenvit, Yupin
APPLICANT: Chart, Richard
APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria sporozoite surface protein
TITLE OF INVENTION: immunogen and gene encoding
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                                                                                                                            Length 4673;
                                                                                                                                                                                                                                                                                                                                                                                                                            324 AAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTT 371
                                                                                                                                                                       80; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: A. David Spevack
STREET: NMRDC Building 1 T-12 National Naval
STREET: Medical Center
STREET: Bethesda
STATE: MD
                                                                                                                        Score 40; DB 1;
Pred. No. 0.21;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDION TYPE: FLORPY disk
COMPUTER: FLORPY disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patchtin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00018
FILING DATE: 19920103
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (301) 295-6759
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
CLENGTH: 4673 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9200018 GENERAL INFORMATION:
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TISSUE TYPE: Blood
CELL TYPE: erythrocytic stage
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STRAIN: 17X(NL)
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HYPOTHETICAL: N
                                                                                                                        Query Match 3.1%;
Best Local Similarity 52.4%;
Matches 88; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                ) LOCATION: 718.,31
; OTHER INFORMATION:
US-07-638-431-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
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LIBRARY: Py-1
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PCT-US92-00018-1
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                                                                                  Db 10342 AAAAAAGGAAATTTGTATTGCAATTTATATTTTAAGTGTTTTTTAACAATTGTTGAAA 10283
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard
APPLICANT: Hedstrom, Richard
APPLICANT: Rousmith, Srisin
APPLICANT: Rousmith: Protective malaria sporozoite surface protein
TITLE OF INVENTION: immunogen and gene
TITLE OF INVENTION: immunogen and gene
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: A. David Spewack
STREET: MRRDC Building 1 T-12 National Naval
STREET: Medical Center
CITY: Bethesda
                                          331 AAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTA 390
                                                                                                                               TTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACATGGTCTACAATGGAAAACA 450
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       96; Indels
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  0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.24
CURRENT APPLICATION DATA:
FILING DATE: 19910110
CLASSIFICATION: 424
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Patent No. 5198535
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STRAIN: 17X(NL)
DEVELOPMENTAL STAGE: erythrocy
TISSUE TYPE: Blood
CELL TYPE: erythrocytic stage
IMMEDIATE SOURCE:
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NAME: Spewack, Avrom D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
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98; Conservative
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STRANDEDNESS: double
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Matches
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                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                         ch 3.1%; Score 40; DB 5; Length 4673;
1 Similarity 52.4%; Pred. No. 0.21;
88; Conservative 0; Mismatches on - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Michalmore, Richard W.
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CONFESTIONERAL ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                             324 AAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTT 371
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COMPUTER: IEM PC compatible
SOFTWARE: PETENT Release #1.0, Ver
SOFTWARE: PETENT Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION BOTA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTATION NUMBER: 38,440
REGISTATION NUMBER: 33070-0788
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 109:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , LOCATION: 1..5829
; OTHER INFORMATION: /note= "RG2K"
US-09-004-838-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 109, Application US/09004838 Patent No. 6350933
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                        ) NAME/KEY: CDS
; LOCATION: 718..3195
; OTHER INFORMATION:
PCT-US92-00018-1
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STATE: California
CLONE: Py10.1111 FEATURE:
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US-09-004-838-109/c
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                                                               209 TCTGTTCTTCTTATTTGTGCATATTTTTATTGTTGTTTACTGATTATACGAGTAGTTATA 268
                                 Gaps
                                                                                                                                                                                                                                                                                                                                     449 CAGTGCTTTGTACGACTATATACGCGATGTGTGGCTACAACATAAGACAATATAGT 504
 DB 4; Length 5829;
Score 40; DB 4; Length 582
Pred. No. 0.24;
0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                7, 2002, 10:48:43
 3.1%;
   Query Match 3.1:
Best Local Similarity 45.9
Matches 136; Conservative
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Job time: 86.9851 secs
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BH25515 RXL1BAM00
AA2921021 1006023E0
AA028053 945007002
AL098595 Drosophil
AL066051 Drosophil
BH255739 LDH5BAM00
AL103998 Drosophil
BE55739 LDH5BAM00
AL103998 Drosophil
BE552390 HYSKEM00
AC251130 F2616-Sp6
AC071298 Drosophil
AL052719 Drosophil
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AL055199 Drosophil
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AL055199 Drosophil
AL055199 Drosophil
AL055199 Drosophil
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                                                                                                                                                                                                                                        US-09-905-558C-16
1309
1 ccatcgctgctttgtctac.....caagggaaagtgatcccatg 1309
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                            13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         OM nucleic - nucleic search, using sw model
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AW928051
AW928053
CNS0106X
AU087781
CNS014D0
AC180808W
AC2046300
AC18089
AC21130
CNS006VB
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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em_tc:*
gb_est1:*
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Match Length DB
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Perfect score:
Sequence:
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AL071865 Drosophil BG852371 1024034A0 AL063921 Drosophil BH255629 LDH5BAM00 AL071865 Drosophil B1959718 HVSME1002 AL175696 Tetraodon AL108704 Drosophil BM163977 EST56550 AL077789 Drosophil AL077804 Drosophil B195364 HVSMEM001 AL256132 AL536132 AL100502 Drosophil AL107841 Drosophil AL107846 Drosophil AL107846 Drosophil AL10785 Drosophil AL10785 Drosophil AL10735 Drosophil AL10735 Drosophil AL10735 Drosophil AL07175 Drosophil AL07175 Drosophil AL07175 Drosophil AL07176 Drosophil BG004199 QV4-GN012 BG41241 GA_EA001 BG641241 GA_EA001 BM166596 EST571119 BM166596 EST571119	ALIGNMENTS BH255115 N RXL1BAM0001A01r Zea mays L. XL1 methyl filtration maize root genomic shotgun library Zea mays genomic clone RXL1BAM0001A01r, DNA sequence. BH255115 BH
CNSOODBKY BCB52371 BCNSOODSY CNSOODSY CNSOODSY CNSO17KE CNSO17KE CNSO17KE CNSO17KE CNSOOSJ CNS	BH255115 RXLIBBAMOOD1AOIr Zea mays L. XLI methy genomic shotgun library Zea mays Ges mays. BH255115.1 GI:17150008 S.Zea mays. Zea mays. Zea mays. Sea mays. Lucatooddeae; Andropogoneae; Zea mays. Sibrardophyta; Magnonlophyta; Lillops Spermatophyta; Mainophyta; Lillops Spermatophyta; Mainophyta; Lillops Sibrardophyta; Mainophyta; Lillops Sibrardophyta; Mainophyta; Lillops Sibrardophyta; Lee,M.C., Yang,T.J., Genomic shotgun library from maize Unpublished (2001) Contact: Wing RA. Clemson University Genomics Institute Clemson University Genomics shotgun library and Migh quality sequence stop: 374. Tel: 864 656 7288 Fax: 864 656 4293 Fax: 864 656 4293 Fax: 864 656 4293 Ingenomic shotgun library and Lity sequence stop: 374. Actain="mays" /db_wref="taxon:4577" /db_wref="taxon:4577" /db_wref="taxon:4577" /db_wotgun" /tissue_type="Rotin" /db_wote-"xLiblue" /dlab_host="XLiblue" /dlab_wote-"XLiblue"
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928 926 926 928 928 928 1101 1101 1101 1101 1101 1101 1101 11	BH255115 RXLIBAM0001A01r Zea mays L genomic shotgun library Zea sequence. BH355115. GI:17150008 GSS. Zea mays. Zea mays Lea mays Lolacy Panicoideae; Andropp 1 (bases 1 to 374) Rim, S.W., Yu, X., Lee, M.C., and Wing, R.A. Genomic shotgun library frc Unpublished (2001) Contact: Wing RA Clemson University Genomics Clemson University 100 Jordan Hall, Clemson, 8 Tel: 864 656 4293 Email: rwingeclemson.edu Seq primer. AATTAACCCTACTY (class: shotgun High quality sequence stop) High quality sequence stop Class: shotgun High quality sequence stop Abarea may Astrain="RXLIBAM000" Clone="RXLIBAM000" Clone="RXLIBAM000" Clone="RXLIBAM000" Clone="RXLIBAM000" Clone="RXLIBAM000" Clone="RXLIBAM000" Clone="RXLIBAM000" Clone="XLIBAM000" Clone
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/organism="zea mays"

/organism="zea mays"

/organism="zea mays"

/outivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/clone_lib="1006 - RescueMu Grid G"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="ngl103"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription
                                                                                                                                                                        3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V.
Department of Biological Sciences
Stanford University
Tel: 650 723 2227
Fex: 650 725 8221
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Methyl-filtration library, Nuclei DNA was digested with Sau3A1, size fractionated and transformed to E.Coli.XL1Blue."
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                                                                                                                                                                                                                                          299 CATACACACGAGATGTCTTGTGTGAATAGAGCCAACGATGTCTTGAGCATCGGTCCCTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGTAGTTATACATACATGCAC - - ATACATATCATCACATATATCACAATATTTTTTTAA 315
                                                                                                                                                                                                                  78 CCGTTCGAGTGACTGCATGGCGTACATCTTTCTGCATCGACTTTGTACGGCTACATCGAA 137
                                                                                                                                                                                                                                                                                                   138 CATATACACGAGATGTCTCGTGTGAATAGAGTCACTAATGCCTTAAGCATCGGTTACTCC 197
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                                                                                                                                 DB 12; Length 374;
                                                                                                                                                                          48; Indels
                                                                                                                                 Score 149.2; DB 1
Pred. No. 5.2e-21;
                                                                                                                                                                          0; Mismatches
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Reverse complemented post-ligation
Plate: 1006023 row: 39
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Cocation/Qualifiers
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79.9%;
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Walbot, V.
                                                                   64 c
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TITLE
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COMMENT
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units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B capls were transformed and then screened on LB plates with a screened on LG plates with the Screened plates with t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 bp mRNA linear EST 30-MAY-2000 94507002.X1 945 - Mixed adult tissues from Walbot lab, same as 707 AW928053
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Vector: pGAD10; Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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1 (bases 1 to 496)
Walbot,V.
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/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 223;
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Pred. No. 9.9e-16;
0; Mismatches 32; Indels
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Email: walbot@stanford.edu
Plate: 945007 row: D column: 02.
Location/Qualifiers
1.496
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/lab_host="DH10B"
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/cultivar="W23"
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Best Local Similarity 82.4%;
Matches 154; Conservative
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Unpublished (1999)
Contact: Walbot V
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Email: jwatanabdanage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUO87/81 Sugano Malaria cDNA library Plasmodium falciparum cDNA clone XPFn5810, mRNA sequence.
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                            НАНМНИТМНИМНИМТИНИТУНММИМНТИНМНТИТНИМННИНИНИНИНИТНИТИТИТНИ 908
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (basea I to 500)
Watanabe,J., Saski,M., Suzuki,Y. and Sugano,S.
FULL-malaria: a database for a full-length enriched cDNA lib from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
                                                                                             329 IAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACC
                                                                                                                                            307 HWMWAMMINTHIMHMINATMINATMINATHHHHHMINTMINTHIHHHMCTYYYMTHTH
                                                                                                                                                                                                                                   389 TATTCTACATTGTTCTATTTCGAATTTCACTCTATAAACAACATAGTCTACAATGGAAAA
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Contact: Junichi Watanabe
Contact: Junichi Watanabe
Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Far: 81-3-5449-5578
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BP 191 91006 EVRY cedex - FRANCE (E-mail : Seqrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC ilbrary (Dros BAC) was made by Alain Billaud at CEPH (Centre of Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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1 Similarity 19.2%; Pred. No. 0.05;
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                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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ATACATATCATCACATATATCACAATATTTTCTAAATTAAAATTAAAACTAAAAATGACT 339
                     400 GITCTATITCGAATITCACTCTATAAACAACATAGICTACAAIGGAAAACAGIGCTIIGT 459
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
                                                                                                                                                                340 AAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAACTTTACCTATTCTACATT
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N09"
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Matches 115;
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/db_xref="taxon.4577"
/clone="LDH5BAM0003C03f"
/clone="LDH5BAM0003C03f"
/clone=llb="Zea mays L. DH5alpha methy filtration maize
leaf genomic shotgun library"
/tissue_type="Leaf"
/lab_host="DH5alpha"
/note="Vector: pCUGIblu-1; Site_1: Sau3Al; Site_2: Sau3Al;
Methyl-filtration library, Nuclei DNA was digested with
Sau3Al, size fractionated and transformed to
E.Coli.DH5alpha."
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                                        741 GSGGSGCSSCSSCSCGCGSSGCGSCGCCCSCGCSCGCSSGCGSCGCSGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Wing RA
Colmson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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TASWITBIACSMITACISAYASYIHTAMTAIATATAAWHYIMWAITHIYAHCATA 936
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                                                                                                                                                                              Oryza sativa.
Oryza sativa
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                                                  RESULT 9
AZ046300/c
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COMMENT
            880
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                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence SP6 end of BAC fly), genomic survey from Drosophila melanogaster (fruit AL103998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: segrefégenoscope.ons.fr web: www.genoscope.ons.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -: This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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296 T----ACACATGCACGTAAATGTCATCACATATTTTATGCAATGTTTTTGGATTAAAT 350
                                                                                                     323 TAAAACTAAAAATGACTAAATTTCTAACACCAACGACATTGTAATGTTTTCTCCAACAAC 382
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1058)
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                                             TTATACATACATGCACATATCATCATCACATATATCACAATAT-TTTTCTAAATTAAAT
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/plasmid-"pbeloBA111"
/db_xref-"taxon:7227"
/clone_lib-"DrosBAC"
/clone="BACN11117"
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32.9%; Pred. No. 0.17;
ive 65; Mismatches 94;
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Best Local Similarity
------ 78; Conserve
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//issue_ild=lib=loud kice bac Library (ECOKI) .
//Lissue_tld="Lough kice bac Library (ECOKI; Site_1: ECOKI; Alab_host="E. coli DH10B"
//Abb_host="E. coli DH
                  16-MAR-2000
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Epermatophyta; Bernatophyta; Epermatophyta; Epermatophyta; Enganoliophyta; Liliopsida; Poales; Poaceae; Erhartoideae; Oryzeae; Oryza.

1 (bases 1 to 745)

1 (bases 1 to 745)

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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AZ046300 745 bp DNA linear GSS 16-MAR-2 nbeb0091L15r CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone OSJNBb0091L15r, DNA sequence.
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/cultivar="Ripponbare"
/db_xref="taxon:4530"
/clone="OSJNBD0091L15r"
/clone=lib="CUGI Rice BAC Library (ECORI)"
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Pred. No. 0.19;
0; Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4298 Email: rwingclemson.edu Seq primer: GCTATTTAGGTGACATATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 213.
Location/Qualifiers
1. 745
/organism="Oryza sativa"
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ilarity 36.7%;
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881 551

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B18 bp mRNA linear EST 19-OCT-2001 HVSMEm0006C23f Hordeum vulgare green seedling EST library HVCDNA0014 (Blumeria infected) Hordeum vulgare cDNA clone HVSMEm0006C23f, mRNA sequence.
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Sperimatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1. (bases 1 to ATR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 818) Wing, R. Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D., Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R. and Main, D. Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected Morex (compatible) seedling
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/cultivar="Morex"
/db_xef="taxon:4513"
/clone="HVSMEM0006673f"
/clone="HVSMEM0006673f"
/clone="HVSMEM0006673f"
/clone="Lye="taxon:4513f"
/clone="HVSMEM0006673f"
/clone="HVSMEM0006673f"
/clone="HVSMEM0006673f"
/clone="HVSMEM000673f"
/clone="HVSMEM000675f"
/clone="HVSMEM0
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                                                                    SC 29634, USA
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Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 808.
Location/Qualifiers
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Total hq bases = 224
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Unpublished (2001)
Contact: Wing RA
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Submitted (02-AuG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpeségac.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG130889.1 GI:16660054
GGS; GSS (genome survey sequence).
BAR troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAR Library clone:PTB-142M17.F.
Pan troglodytes
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Pan troglodytes DNA, clone: PTB-142M17.F, genomic survey sequence.
AG130889
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
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29 others
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4.2%; Score 55.2; DB 12;
Best Local Similarity 47.0%; Pred. No. 0.21;
Matches 171; Conservative 0; Mismatches 193;
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/clone_lib="PTB Chimpanzee Male
a 63 c 638 g 24 t
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/db_xref="taxon:9598"
/clone="PTB-142M17.F"
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Whose the plants were greenhouse grown in the R Wise lab at lowa State University, Ames, IA: 7 day old green seedlings were infected with isolate 587 of Blumerla graminis f. sp. hordel, and leaves were harvested 24, 48 and 72 hr post-incoulation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 142 c 556 g 46 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCCTGTCGGCCCTTTGTTTATTCATCCCGAAATCTCATCTGCCCCCACGGCCGACTGC 1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     above. For more details on library preparation and
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49.8%; Pred. No. 0.34;
tive 0; Mismatches 138;
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BAC End Sequences at ATGC Unpublished (1997)
Contact: Ecker J.
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Matches 137; Conserva
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CNSOOFVE 1101 bp DNA 11near GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR32P18 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 1910 GEVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                                                                                                                                                                                     /cloue__________/
/sax="hermaphrodite"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
no 90 q 259 t 3 others
             University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
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Muscomorpha; Ephydroldea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                          thaliana"
                                                                               Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seg primer: Sp6
Class: BAC ends.
Vrabidopsis Thaliana Genome Center
                                                                                                                                                                                                                   1. .798
/organism="Arabidopsis
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/clone="F26H6"
/clone_llb="IGF"
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LOSD Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACRIBLIA of RPCI-98 library from Drosophila melanogaster (fruit
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                 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
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Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila genome Project (BDG The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Best Local Similarity 29.1%;
Matches 102; Conservative 8
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1 (bases 1 to 945)

1 (bases 1 to 945)

1 (bases 1, Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouncau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw 8p, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1101;
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/db_xref="taxon:7227"
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VL Submitted (12-APR-2000) to the EWBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr?Tetraodon.

i coation/Qualifiers
Irce / Organism="Tetraodon nigroviridis" / Ab_xref="taxon:99883"
/ Clone="10,111" / Clone="112" / Clone="112" / Clone="112" / Clone="Genoscope sequence ID: COBGIOICDIILP1-end: T7"

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